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(54) Title: CUTINASE VARIANTS

(57) Abstract

Variants of fungal cutinases have improved thermostability. The variants comprise substitution of one or more amino acid residues near the N-terminal in the amino acid sequence or in the three-dimensional structure of the cutinase.

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CUTINASE VARIANTS

FIELD OF THE INVENTION

The present invention relates to a cutinase variant, more particularly to a cutinase variant having improved thermostability. The invention also relates to a DNA sequence encoding the variant, a vector comprising the DNA sequence, a transformed host cell harboring the DNA sequence or the vector, to a method of producing the variant, and to use of the variant.

BACKGROUND OF THE INVENTION

Cutinases are lipolytic enzymes capable of hydrolyzing the substrate cutin. Cutinases are known from various fungi (P.E. Kolattukudy in "Lipases", Ed. B. Borgström and H.L. Brockman, Elsevier 1984, 471-504). The amino acid sequence and the crystal structure of a cutinase of *Fusarium solani pisi* have been described (S. Longhi et al., Journal of Molecular Biology, 268 (4), 779-799 (1997)). The amino acid sequence of a cutinase from *Humicola insolens* has also been published (US 5,827,719).

A number of variants of the cutinase of *Fusarium solani pisi* have been published: WO 94/14963; WO 94/14964; Appl. Environm. Microbiol. 64, 2794-2799, 1998; Proteins: Structure, Function and Genetics 26, 442-458, 1996; J. of Computational Chemistry 17, 1783-1803, 1996; Protein Engineering 6, 157-165, 1993; Proteins: Structure, Function, and Genetics 33, 253-264, 1998; J. of Biotechnology 66, 11-26, 1998; Biochemistry 35, 398-410, 1996.

Fungal cutinases may be used in the enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) fibers (WO 97/27237). However, it is desirable to improve the thermostability of known fungal cutinases to allow a higher process temperature.

SUMMARY OF THE INVENTION

The inventors have found certain variants of fungal cutinases having improved thermostability.

Accordingly, the invention provides a variant of a parent fungal cutinase comprising substitution of one or more amino acid residues which is located:

a) within 17 Å from the location of the N-terminal amino acid (as calculated from amino acid residues in a crystal structure), and/or

b) within 20 positions from the N-terminal amino acid.

The invention also provides a DNA sequence encoding the variant, an expression vector comprising the DNA sequence, a transformed host cell harboring the DNA sequence or the expression vector, a method of producing the variant, processes using the variant and a detergent composition comprising the variant.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 gives the coordinates for the 3D structure of the cutinase of *H. insolens*.

Fig. 2 is a computer model showing the three-dimensional structures of the cutinases from *F. solani pisi* (left) and *H. insolens* (right). Different colors have been used to identify the N-terminal amino acid and zones of 12 Å and 17 Å diameter around this.

Figs. 3-6 illustrate the hydrolysis of c3ET. Details are given in the Examples.

DETAILED DESCRIPTION OF THE INVENTION

Fungal cutinase

The parent cutinase is a fungal cutinase, such as a filamentous fungal cutinase, e.g. native to a strain of *Humicola* or *Fusarium*, specifically *H. insolens* or *F. solani pisi*, more specifically *H. insolens* strain DSM 1800.

The amino acid sequence of the cutinase of *H. insolens* strain DSM 1800 and the DNA sequence encoding it are shown as SEQ ID NO: 2 and SEQ ID NO: 1 of US 5,827,719. The numbering system used herein for the *H. insolens* cutinase is based on the mature peptide, as shown in said SEQ ID NO: 2.

The amino acid sequence of the cutinase of *F. solani pisi* is shown as the mature peptide in Fig. 1D of WO 94/14964. The numbering system used herein for

the *F. solani pisi* cutinase is that used in WO 94/14964; it includes the pro-sequence shown in said Fig. 1D; thus, the mature cutinase is at positions 16-214.

The parent cutinase may have an amino acid sequence which is at least 50 % (particularly at least 70 % or at least 80 %) homologous to the cutinase of *H. insolens* strain DSM 1800. The parent cutinase may particularly be one that can be aligned with the cutinase of *H. insolens* strain DSM 1800.

Nomenclature for amino acids and alterations

The specification and claims refer to amino acids by their one-letter codes. A particular amino acid in a sequence is identified by its one-letter code and its position, e.g. Q1 indicates Gln (glutamine at position 1, i.e. at the N-terminal.

The nomenclature used herein for defining substitutions is basically as described in WO 92/05249. Thus, R51P indicates substitution of R (Arg) at position 51 with P (Pro).

Homology and alignment

For purposes of the present invention, the degree of homology may be suitably determined according to the method described in Needleman, S.B. and Wunsch, C.D., (1970), Journal of Molecular Biology, 48, 443-45, with the following settings for polypeptide sequence comparison: GAP creation penalty of 3.0 and GAP extension penalty of 0.1. The determination may be done by means of a computer program known such as GAP provided in the GCG program package (Program Manual for the Wisconsin Package, Version 8, August 1994, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711).

Two given sequences can be aligned according to the method described in Needleman (*supra*) using the same parameters. This may be done by means of the GAP program (*supra*).

Three-dimensional structure of cutinase

The structure of the cutinase of *H. insolens* was solved in accordance with the principle for X-ray crystallographic methods as given, for example, in X-Ray Structure Determination, Stout, G.K. and Jensen, L.H., John Wiley & Sons, Inc. NY, 1989. The structural coordinates for the solved crystal structure at 2.2 Å resolution

using the isomorphous replacement method are given in Fig. 1 in standard PDB format (Protein Data Bank, Brookhaven National Laboratory, Brookhaven, CT).

The structure of the cutinase of *F. solani pisi* is described in Martinez et al. (1992) Nature 356, 615-618. The 3D structures of the cutinases of *F. solani pisi* and *H. insolens* are compared as a computer model in Fig. 2.

It should be noted that the overall three-dimensional structures of fungal cutinases are very similar and have been shown by X-ray crystallography to be highly homologous. The similarities between the cutinases from *F. solani pisi* and *H. insolens* are clearly apparent from the computer model in Fig. 2. Therefore, modifications of the type indicated for one fungal cutinase will also be functional for other fungal cutinases.

Substitution near N-terminal

The variant of the invention has one or more amino acid substitutions in the vicinity of the N-terminal. The substitution is within a distance of 17 Å (e.g. within 12 Å) and/or within 20 positions (e.g. within 15 positions) of the N-terminal. The distance from the N-terminal is to be calculated between the Cα atom of the amino acids, and is calculated from an amino acid in a crystal structure (i.e. visible in the X-ray structure).

In the cutinase of *H. insolens* strain DSM 1800, the two N-terminal amino acids (Q1 and L2. i.e. Gln and Leu at positions 1 and 2) are not visible in the X-ray structure, so the distance is to be calculated from amino acid G3. Amino acids within 17 Å include positions 3-12, 18, 20-60, 62-64, 82, 85-86, 100-108, 110-111, 130-132, 174, 176-182, 184-185, 188, and 192. Those within 12 Å include positions 3-8, 22-27, 30-47, 53-59, 102, 177, and 180-181.

In the cutinase of *F. solani pisi*, the N-terminal amino acid G17 is visible in the X-ray structure. Amino acids within 17 Å include positions 17-26, 34-75, 77-79, 101, 115, 117-119, 147, 191-197, 199-200, and 203. Those within 12 Å include positions 17-22, 38, 40, 45-58, 60, 65, and 70-72.

The variants of the invention have improved thermostability compared to the parent enzyme. The thermostability may be determined from the denaturation tem-

perature by DSC (differential scanning calorimetry), e.g. as described in an example, e.g. at pH 8.5 with a scan rate of 90 K/hr. The variants may have a denaturation temperature which is at least 5°C higher than the parent enzyme.

The total number of substitutions in the above regions is typically 1-10, e.g. 1-5 substitutions in the above regions. In addition, the cutinase variant of the invention may optionally include other modifications of the parent enzyme, typically 10 or fewer, e.g. 5 or fewer alterations (substitutions, deletions or insertions) outside of the above regions. Thus, the total amino acid sequence of the variant typically 1-20, e.g. 1-10 alterations compared to the parent cutinase.

Solvent accessible surface

One or more of the substitutions may be made at an exposed amino acid residue, i.e. an amino acid residue having a solvent accessible surface. This can be calculated by the "dssp" program (version October 1988) described in W. Kabsch and C. Sander, Biopolymers, 22 (1983) pp. 2577-2637.

In the cutinase of *H. insolens* strain DSM 1800, the following amino acids lie within 17 Å of G3 at the N-terminal and have a solvent accessible surface greater than 0: 3-12, 18, 26-33, 36-38, 40-45, 47-56, 59-60, 62-64, 82, 85-86, 104-105, 174, 176-179, 181-182, 192.

Specific substitutions

The substitution near the N-terminal may specifically be one that increases the electrical charge, i.e. a substitution of a negatively charged amino acid with a neutral or positively charged amino acid or substitution of a neutral amino acid with a positively charged amino acid. Thus, a negative amino acid residue at a position corresponding to position E6, E10, E30, E47 D63, E82 and/or E179 in the cutinase of *Humicola insolens* strain DSM 1800 may be substituted by a neutral or positive amino acid, e.g. R, K, Y, H, Q or N. Some specific substitutions are those corresponding to E6Q/N, E10Q/N, E47K/R or E179Q/N. Also, a neutral amino acid residue at a position corresponding to N7, S11, N44 or N52 in the *H. insolens* cutinase may be substituted by a positive amino acid (R, K or H).

Another example of a substitution near the N-terminal is substitution with a Pro residue, e.g. a substitution corresponding to A14P or R51P in the cutinase of *Humicola insolens* strain DSM 1800.

Specific variants

The following are some examples of variants in the *H. insolens* cutinase. Corresponding variants may be made on the basis of other parent cutinases.

R51P
E6N/Q+ L138I
A14P+ E47K
E47K
E179N/Q
E6N/Q+ E47K+ R51P
A14P+ E47K+ E179N/Q
E47K+ E179N/Q
E47K+ D63N
E6N/Q+ E10N/Q+ A14P+ E47K+ R51P+ E179N/Q
E6N/Q+ A14P+ E47K+ R51P+ E179N/Q
Q1P+ L2V+ S11C+ N15T+ F24Y+ L46I+ E47K

Use of cutinase variant

The cutinase variant of the invention may be used, e.g., for the enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), such as cyclic tri(ethylene terephthalate), abbreviated as c3ET.

In particular, this may be used to remove such cyclic oligomers from polyester containing fabric or yarn by treating the fabric or yarn with the cutinase variant, optionally followed by rinsing the fabric or yarn with an aqueous solution having a pH in the range of from about pH 7 to about pH 11. The treatment of polyester is conveniently carried out above the glass transition temperature of c3ET (about 55°C) and below the glass transition temperature of polyester (about 70°C). Thus, the treatment may suitably be carried out at 50-80°C, e.g. at 60-75°C. The process may be carried out in analogy with WO 97/27237.

The cutinase variant may be used to treat polyester-containing textile. e.g. PET (polymer of ethyleneglycol and terephthalic acid), P3GT (polymer of 1,3-propanediol and terephthalic acid) or a polyester/cotton blend. The treatment may provide benefits to the polyester textile such as improved wear and comfort, increased water permeability, reduced antistatic behavior, improve handle and softness, changed redeposition characteristics and/or color clarification.

The cutinase variant may be used to improve the functional finish of a PET-containing yarn or fabric by a treatment with the cutinase variant, followed by a treatment with a finishing agent such as a softener, an anti-crease resin, an anti-static agent, an anti-soiling agent or agents to impair wrinkle-free, permanent press ior fire resistance effects. The treatment with the cutinase variant may increase the number of functional groups in the surface, and this can be used to attach the functional finish. Examples of finishing agents are described in "SENSHOKU SIAGEKAKO BENRAN" published 1998-10-15 by Nihon Seni Sentaa KK.

The cutinase variant of the invention is also useful in detergents, where it may be incorporated to improve the removal of fatty soiling, as described in WO 94/03578 and WO 94/14964. The addition of the cutinase variant to laundry detergent may reduce malodor from cloth which is accumulated during several wash/wear-cycles.

The cutinase variant may also be used for degradation and recycling of polyester such as polycaprolactone (PCL), poly-ethyleneglycol-terephthalate (PET), polylactic acid, polybutylenesuccinate, and poly(hydroxybutiric acid)-co-(hydroxyvaleric acid), e.g. film and bottles, e.g. as described in JP-A 5-344897.

The cutinase variant may also be used for other known applications of lipases and cutinases, for example, in the baking industry (e.g. as described in WO 94/04035 and EP 585988), in the papermaking industry (e.g. for pitch removal, see EP 374700), and in the leather, wool and related industries (e.g. for degreasing of animal hides, sheepskin or wool), and for other applications involving degreasing/defatting. It may be used in immobilized form in the fat and oil industry, as a catalyst in organic synthesis (e.g. esterification, transesterification or ester hydrolysis reactions).

Dyeing polyester

The invention provides a process for dyeing polyester fabric or yarn. In this process, the fabric or yarn is first treated with a cutinase, e.g. 12-48 hours at 50-70°C or 65-70°C, pH 7-10, followed by dyeing with dye, e.g. a reactive dye, a disperse dye or a cationic dye. The reactive dye may be one that reacts with OH or COOH groups, e.g. having the structure Chromophore-NHPh-$SO_2CH_2CH_2OSO_3Na$. The dyeing may be conducted at 40-80°C, e.g. for 20-60 minutes.

The cutinase may be a thermostable cutinase having a thermal denaturation temperature, T_d, at pH 8.5 which is at least 5° higher than the parent cutinase, e.g. 7-10° higher, e.g. a value of 65°C or higher. The measurement may be made by DSC as described in an Example of this specification.

Surfactant

In the treatment of fabric or yarn, a conventional wetting agent and/or a dispersing agent may be used to improve the contact with the enzyme. The wetting agent may be a nonionic surfactant, e.g. an ethoxylated fatty alcohol. A very useful wetting agent is an ethoxylated and propoxylated fatty acid ester such as Berol 087 (product of Akzo Nobel, Sweden).

The dispersing agent may suitably be selected from nonionic, anionic, cationic, ampholytic or zwitterionic surfactants. More specifically, the dispersing agent may be selected from carboxymethylcellulose, hydroxypropylcellulose, alkyl aryl sulfonates, long-chain alcohol sulfates (primary and secondary alkyl sulfates), sulfonated olefins, sulfated monoglycerides, sulfated ethers, sulfosuccinates, sulfonated methyl ethers, alkane sulfonates, phosphate esters, alkyl isothionates, acylsarcosides, alkyltaurides, fluorosurfactants, fatty alcohol and alkylphenol condensates, fatty acid condensates, condensates of ethylene oxide with an amine, condensates of ethylene oxide with an amide, sucrose esters, sorbitan esters, alkyloamides, fatty amine oxides, ethoxylated monoamines, ethoxylated diamines, alcohol ethoxylate and mixtures thereof. A very useful dispersing agent is an alcohol ethoxylate such as Berol 08 (product of Akzo Nobel, Sweden).

Methods for preparing cutinase variants

The cutinase variant of the invention can be prepared by methods known in the art, e.g. as described in WO 94/14963 or WO 94/14964 (Unilever). The following describes methods for the cloning of cutinase-encoding DNA sequences, followed by methods for generating mutations at specific sites within the cutinase-encoding sequence.

Cloning a DNA sequence encoding a cutinase

The DNA sequence encoding a parent cutinase may be isolated from any cell or microorganism producing the cutinase in question, using various methods well known in the art. First, a genomic DNA and/or cDNA library should be constructed using chromosomal DNA or messenger RNA from the organism that produces the cutinase to be studied. Then, if the amino acid sequence of the cutinase is known, labeled oligonucleotide probes may be synthesized and used to identify cutinase-encoding clones from a genomic library prepared from the organism in question. Alternatively, a labeled oligonucleotide probe containing sequences homologous to another known cutinase gene could be used as a probe to identify cutinase-encoding clones, using hybridization and washing conditions of lower stringency.

Yet another method for identifying cutinase-encoding clones would involve inserting fragments of genomic DNA into an expression vector, such as a plasmid, transforming cutinase-negative bacteria with the resulting genomic DNA library, and then plating the transformed bacteria onto agar containing a substrate for cutinase (*i.e.* maltose), thereby allowing clones expressing the cutinase to be identified.

Alternatively, the DNA sequence encoding the enzyme may be prepared synthetically by established standard methods, *e.g.* the phosphoroamidite method described S.L. Beaucage and M.H. Caruthers, (1981), Tetrahedron Letters 22, p. 1859-1869, or the method described by Matthes et al., (1984), EMBO J. 3, p. 801-805. In the phosphoroamidite method, oligonucleotides are synthesized, *e.g.* in an automatic DNA synthesizer, purified, annealed, ligated and cloned in appropriate vectors.

Finally, the DNA sequence may be of mixed genomic and synthetic origin, mixed synthetic and cDNA origin or mixed genomic and cDNA origin, prepared by

ligating fragments of synthetic, genomic or cDNA origin (as appropriate, the fragments corresponding to various parts of the entire DNA sequence), in accordance with standard techniques. The DNA sequence may also be prepared by polymerase chain reaction (PCR) using specific primers, for instance as described in US 4,683,202 or R.K. Saiki et al., (1988), Science 239, 1988, pp. 487-491.

Site-directed mutagenesis

Once a cutinase-encoding DNA sequence has been isolated, and desirable sites for mutation identified, mutations may be introduced using synthetic oligonucleotides. These oligonucleotides contain nucleotide sequences flanking the desired mutation sites. In a specific method, a single-stranded gap of DNA, the cutinase-encoding sequence, is created in a vector carrying the cutinase gene. Then the synthetic nucleotide, bearing the desired mutation, is annealed to a homologous portion of the single-stranded DNA. The remaining gap is then filled in with DNA polymerase I (Klenow fragment) and the construct is ligated using T4 ligase. A specific example of this method is described in Morinaga et al., (1984), Biotechnology 2, p. 646-639. US 4,760,025 discloses the introduction of oligonucleotides encoding multiple mutations by performing minor alterations of the cassette. However, an even greater variety of mutations can be introduced at any one time by the Morinaga method, because a multitude of oligonucleotides, of various lengths, can be introduced.

Another method for introducing mutations into cutinase-encoding DNA sequences is described in Nelson and Long, (1989), Analytical Biochemistry 180, p. 147-151. It involves the 3-step generation of a PCR fragment containing the desired mutation introduced by using a chemically synthesized DNA strand as one of the primers in the PCR reactions. From the PCR-generated fragment, a DNA fragment carrying the mutation may be isolated by cleavage with restriction endonucleases and reinserted into an expression plasmid.

Expression of cutinase variants

According to the invention, a DNA sequence encoding the variant produced by methods described above, or by any alternative methods known in the art, can be expressed, in enzyme form, using an expression vector which typically includes con-

trol sequences encoding a promoter, operator, ribosome binding site, translation initiation signal, and, optionally, a repressor gene or various activator genes.

Expression vector

The recombinant expression vector carrying the DNA sequence encoding a cutinase variant of the invention may be any vector which may conveniently be subjected to recombinant DNA procedures, and the choice of vector will often depend on the host cell into which it is to be introduced. The vector may be one which, when introduced into a host cell, is integrated into the host cell genome and replicated together with the chromosome(s) into which it has been integrated. Examples of suitable expression vectors include pMT838.

Promoter

In the vector, the DNA sequence should be operably connected to a suitable promoter sequence. The promoter may be any DNA sequence which shows transcriptional activity in the host cell of choice and may be derived from genes encoding proteins either homologous or heterologous to the host cell.

Examples of suitable promoters for directing the transcription of the DNA sequence encoding a cutinase variant of the invention, especially in a bacterial host, are the promoter of the *lac* operon of *E.coli*, the *Streptomyces coelicolor* agarase gene *dag*A promoters, the promoters of the *Bacillus licheniformis* α-amylase gene (*amyL*), the promoters of the *Bacillus stearothermophilus* maltogenic amylase gene (*amyM*), the promoters of the *Bacillus amyloliquefaciens* α-amylase (*amyQ*), the promoters of the *Bacillus subtilis* xylA and xylB genes etc. For transcription in a fungal host, examples of useful promoters are those derived from the gene encoding *A. oryzae* TAKA amylase, the TPI (triose phosphate isomerase) promoter from *S. cerevisiae* (Alber et al. (1982), J. Mol. Appl. Genet 1, p. 419-434, *Rhizomucor miehei* aspartic proteinase, *A. niger* neutral α-amylase, *A. niger* acid stable α-amylase, *A. niger* glucoamylase, *Rhizomucor miehei* lipase, *A. oryzae* alkaline protease, *A. oryzae* triose phosphate isomerase or *A. nidulans* acetamidase.

Expression vector

The expression vector of the invention may also comprise a suitable transcription terminator and, in eukaryotes, polyadenylation sequences operably connected to the DNA sequence encoding the α-amylase variant of the invention. Termination and polyadenylation sequences may suitably be derived from the same sources as the promoter.

The vector may further comprise a DNA sequence enabling the vector to replicate in the host cell in question. Examples of such sequences are the origins of replication of plasmids pUC19, pACYC177, pUB110, pE194, pAMB1 and pIJ702.

The vector may also comprise a selectable marker, e.g. a gene the product of which complements a defect in the host cell, such as the *dal* genes from *B. subtilis* or *B. licheniformis*, or one which confers antibiotic resistance such as ampicillin, kanamycin, chloramphenicol or tetracyclin resistance. Furthermore, the vector may comprise *Aspergillus* selection markers such as amdS, argB, niaD and sC, a marker giving rise to hygromycin resistance, or the selection may be accomplished by co-transformation, *e.g.* as described in WO 91/17243.

The procedures used to ligate the DNA construct of the invention encoding a cutinase variant, the promoter, terminator and other elements, respectively, and to insert them into suitable vectors containing the information necessary for replication, are well known to persons skilled in the art (cf., for instance, Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor, 1989).

Host Cells

The cell of the invention, either comprising a DNA construct or an expression vector of the invention as defined above, is advantageously used as a host cell in the recombinant production of a cutinase variant of the invention. The cell may be transformed with the DNA construct of the invention encoding the variant, conveniently by integrating the DNA construct (in one or more copies) in the host chromosome. This integration is generally considered to be an advantage as the DNA sequence is more likely to be stably maintained in the cell. Integration of the DNA constructs into the host chromosome may be performed according to conventional

methods, *e.g.* by homologous or heterologous recombination. Alternatively, the cell may be transformed with an expression vector as described above in connection with the different types of host cells.

The cell of the invention may be a cell of a higher organism such as a mammal or an insect, but is preferably a microbial cell, e.g. a bacterial or a fungal (including yeast) cell.

Examples of suitable bacteria are Gram positive bacteria such as *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus lentus*, *Bacillus brevis*, *Bacillus stearothermophilus*, *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus coagulans*, *Bacillus circulans*, *Bacillus lautus*, *Bacillus megaterium*, *Bacillus thuringiensis*, or *Streptomyces lividans* or *Streptomyces murinus*, or gramnegative bacteria such as *E.coli*. The transformation of the bacteria may, for instance, be effected by protoplast transformation or by using competent cells in a manner known *per se*.

The yeast organism may favorably be selected from a species of *Saccharomyces* or *Schizosaccharomyces*, *e.g. Saccharomyces cerevisiae*.

The host cell may also be a filamentous fungus *e.g.* a strain belonging to a species of *Aspergillus*, most preferably *Aspergillus oryzae* or *Aspergillus niger*, or a strain of *Fusarium*, such as a strain of *Fusarium oxysporium*, *Fusarium graminearum* (in the perfect state named *Gribberella zeae*, previously *Sphaeria zeae*, *synonym with Gibberella roseum and Gibberella roseum* f. sp. *cerealis)*, or *Fusarium sulphureum (*in the prefect state named *Gibberella puricaris*, synonym with *Fusarium trichothecioides*, *Fusarium bactridioides*, *Fusarium sambucium*, *Fusarium roseum*, and *Fusarium roseum var. graminearum)*, *Fusarium cerealis (*synonym with *Fusarium crokkwellnse*), or *Fusarium venenatum*.

In a preferred embodiment of the invention the host cell is a protease deficient or protease minus strain.

This may for instance be the protease deficient strain *Aspergillus oryzae* JaL 125 having the alkaline protease gene named "alp" deleted. This strain is described in WO 97/35956 (Novo Nordisk).

Filamentous fungi cells may be transformed by a process involving protoplast formation and transformation of the protoplasts followed by regeneration of the cell wall in a manner known per se. The use of *Aspergillus* as a host micro-organism

is described in EP 238 023 (Novo Nordisk A/S), the contents of which are hereby incorporated by reference.

Production of cutinase variant by cultivation of transformant

The invention relates, *inter alia*, to a method of producing a cutinase variant of the invention, which method comprises cultivating a host cell under conditions conducive to the production of the variant and recovering the variant from the cells and/or culture medium.

The medium used to cultivate the cells may be any conventional medium suitable for growing the host cell in question and obtaining expression of the cutinase variant of the invention. Suitable media are available from commercial suppliers or may be prepared according to published recipes (*e.g.* as described in catalogues of the American Type Culture Collection).

The cutinase variant secreted from the host cells may conveniently be recovered from the culture medium by well-known procedures, including separating the cells from the medium by centrifugation or filtration, and precipitating proteinaceous components of the medium by means of a salt such as ammonium sulphate, followed by the use of chromatographic procedures such as ion exchange chromatography, affinity chromatography, or the like.

Expression of variant in plants

The present invention also relates to a transgenic plant, plant part or plant cell which has been transformed with a DNA sequence encoding the variant of the invention so as to express and produce this enzyme in recoverable quantities. The enzyme may be recovered from the plant or plant part. Alternatively, the plant or plant part containing the recombinant enzyme may be used as such.

The transgenic plant can be dicotyledonous or monocotyledonous, for short a dicot or a monocot. Examples of monocot plants are grasses, such as meadow grass (blue grass, Poa), forage grass such as festuca, lolium, temperate grass, such as Agrostis, and cereals, e.g. wheat, oats, rye, barley, rice, sorghum and maize (corn).

Examples of dicot plants are tobacco, legumes, such as lupins, potato, sugar beet, pea, bean and soybean, and cruciferous (family Brassicaceae), such as cauliflower, oil seed rape and the closely related model organism Arabidopsis thaliana.

Examples of plant parts are stem, callus, leaves, root, fruits, seeds, and tubers. In the present context, also specific plant tissues, such as chloroplast, apoplast, mitochondria, vacuole, peroxisomes and cytoplasm are considered to be a plant part. Furthermore, any plant cell, whatever the tissue origin, is considered to be a plant part.

Also included within the scope of the invention are the progeny of such plants, plant parts and plant cells.

The transgenic plant or plant cell expressing the variant of the invention may be constructed in accordance with methods known in the art. In short the plant or plant cell is constructed by incorporating one or more expression constructs encoding the enzyme of the invention into the plant host genome and propagating the resulting modified plant or plant cell into a transgenic plant or plant cell.

Conveniently, the expression construct is a DNA construct which comprises a gene encoding the enzyme of the invention in operable association with appropriate regulatory sequences required for expression of the gene in the plant or plant part of choice. Furthermore, the expression construct may comprise a selectable marker useful for identifying host cells into which the expression construct has been integrated and DNA sequences necessary for introduction of the construct into the plant in question (the latter depends on the DNA introduction method to be used).

The choice of regulatory sequences, such as promoter and terminator sequences and optionally signal or transit sequences is determined, eg on the basis of when, where and how the enzyme is desired to be expressed. For instance, the expression of the gene encoding the enzyme of the invention may be constitutive or inducible, or may be developmental, stage or tissue specific, and the gene product may be targeted to a specific tissue or plant part such as seeds or leaves. Regulatory sequences are eg described by Tague et al, Plant, Phys., 86, 506, 1988.

For constitutive expression the 35S-CaMV promoter may be used (Franck et al., 1980. Cell 21: 285-294). Organ-specific promoters may eg be a promoter from

storage sink tissues such as seeds, potato tubers, and fruits (Edwards & Coruzzi, 1990. Annu. Rev. Genet. 24: 275-303), or from metabolic sink tissues such as meristems (Ito et al., 1994. Plant Mol. Biol. 24: 863-878), a seed specific promoter such as the glutelin, prolamin, globulin or albumin promoter from rice (Wu et al., Plant and Cell Physiology Vol. 39, No. 8 pp. 885-889 (1998)), a *Vicia faba* promoter from the legumin B4 and the unknown seed protein gene from *Vicia faba* described by Conrad U. et al, Journal of Plant Physiology Vol. 152, No. 6 pp. 708-711 (1998), a promotter from a seed oil body protein (Chen et al., Plant and cell physiology vol. 39, No. 9 pp. 935-941 (1998), the storage protein napA promoter from Brassica napus, or any other seed specific promoter known in the art, eg as described in WO 91/14772. Furthermore, the promoter may be a leaf specific promoter such as the rbcs promoter from rice or tomato (Kyozuka et al., Plant Physiology Vol. 102, No. 3 pp. 991-1000 (1993), the chlorella virus adenine methyltransferase gene promoter (Mitra, A. and Higgins, DW, Plant Molecular Biology Vol. 26, No. 1 pp. 85-93 (1994), or the aldP gene promoter from rice (Kagaya et al., Molecular and General Genetics Vol. 248, No. 6 pp. 668-674 (1995), or a wound inducible promoter such as the potato pin2 promoter (Xu et al, Plant Molecular Biology Vol. 22, No. 4 pp. 573-588 (1993).

A promoter enhancer element may be used to achieve higher expression of the enzyme in the plant. For instance, the promoter enhancer element may be an intron which is placed between the promoter and the nucleotide sequence encoding the enzyme. For instance, Xu et al. *op cit* disclose the use of the first intron of the rice actin 1 gene to enhance expression.

The selectable marker gene and any other parts of the expression construct may be chosen from those available in the art.

The DNA construct is incorporated into the plant genome according to conventional techniques known in the art, including *Agrobacterium*-mediated transformation, virus-mediated transformation, micro injection, particle bombardment, biolistic transformation, and electroporation (Gasser et al, Science, 244, 1293; Potrykus, Bio/Techn. 8, 535, 1990; Shimamoto et al, Nature, 338, 274, 1989).

Presently, *Agrobacterium tumefaciens* mediated gene transfer is the method of choice for generating transgenic dicots (for review Hooykas & Schilperoort, 1992.

Plant Mol. Biol. 19: 15-38), however it can also be used for transforming monocots, although other transformation methods are generally preferred for these plants. Presently, the method of choice for generating transgenic monocots is particle bombardment (microscopic gold or tungsten particles coated with the transforming DNA) of embryonic calli or developing embryos (Christou, 1992. Plant J. 2: 275-281; Shimamoto, 1994. Curr. Opin. Biotechnol. 5: 158-162; Vasil et al., 1992. Bio/Technology 10: 667-674). An alternative method for transformation of monocots is based on protoplast transformation as described by Omirulleh S, et al., Plant Molecular biology Vol. 21, No. 3 pp. 415-428 (1993).

Following transformation, the transformants having incorporated the expression construct are selected and regenerated into whole plants according to methods well-known in the art.

MATERIALS AND METHODS

Plasmids

pJSO026

This is a *S. cerevisiae* expression plasmid described in WO 97/07205 and in J.S.Okkels, (1996) "A URA3-promoter deletion in a pYES vector increases the expression level of a fungal lipase in Saccharomyces cerevisiae. Recombinant DNA Biotechnology III: The Integration of Biological and Engineering Sciences, vol. 782 of the Annals of the New York Academy of Sciences).

pFuku83

This is a yeast and E. coli shuttle vector for expression of the H. insolens cutinase under the control of a TPI promoter, constructed from pJSO026.

Substrate

BETEB

Terephthalic acid bis(2-hydroxyethyl)ester dibenzoate is herein abbreviated as BETEB (benzoyl-ethylene-terephthalic-ethelene-benzoate). It was prepared from terephthalic acid bis (2-hydroxyethyl) ester and benzoic acid.

Lipase activity (LU)

A substrate for lipase is prepared by emulsifying tributyrin (glycerin tributyrate) using gum Arabic as emulsifier. The hydrolysis of tributyrin at 30 °C at pH 7 is followed in a pH-stat titration experiment. One unit of lipase activity (1 LU) equals the amount of enzyme capable of releasing 1 µmol butyric acid/min at the standard conditions.

Differential scanning calorimetry (DSC)

Sample and reference solutions are carefully degassed immediately prior to loading of samples into the calorimeter (reference: buffer without enzyme). Sample and reference solutions (approx. 0.5 ml) are thermally pre-equillibrated for 20 minutes at 5°C. The DSC scan is performed from 5 C to 95 C at a scan rate of approx. 90 K/hr. Denaturation temperatures are determined at an accuracy of approx. +/- 1 C. A VP-DSC from MicroCal Inc. is suitable for the experiments.

Methods

PCR conditions

step 1: 94° C, 120 sec.
step 2: 94° C, 60 sec
step 3: 50° C, 60 sec
step 4: 72° C, 150 sec.
Go to step 2, 35 cycles
step 5: 72° C, 480 sec.
Step 6: 4° C, for ever

EXAMPLES

Example 1: Preparation of cutinase variants

A DNA sequence encoding *H. insolens* cutinase was obtained as described in US 5,827,719 (Novo Nordisk) and was found to have the DNA sequence shown in SEQ ID NO: 1 therein.

Variants were prepared by localized random mutagenesis and selection of positive clones by incubation at 60°C for 1 day on BETEB plates. The BETEB plates contained 200 ml/l of 500 mM glycine buffer (pH 8.5), 1.25 g/l of BETEB (dissolved in hot ethanol) and 20 g/l of agar.

Three positive variants were isolated, and their amino acid sequence was determined. They were found to have the following modifications, compared to the parent *H. insolens* cutinase:

A14P + E47K

E47K

E179Q

Example 2: Site directed mutation

A variant of the *H.* insolens cutinase having the substitutions E6Q+ E47K+ R51P was prepared as follows:

A pair of PCR primers were designed so as to introduce amino acid substitutions, making use of the existed restriction enzyme sites nearby, as follows (an asterisk indicates an introduced mutation):

Upper primer: E6Q F

cgg cag ctg gga gcc atc c*ag aac

Pvu II

Lower primer: E47K,R51P

cgc cct gga tcc aga tgt tcg* gga tgt ggg act t*aa ggc

*Bam*H I

PCR was run using these primers and pFukuNL83 as a template under the PCR condition described above.

The obtained PCR fragment was purified by Clontech Spincolumn and digested with *Pvu* II and *Bam*H I.

The resultant fragment was gel-purified and ligated to pFukuNL83 which had been digested with the same restriction enzyme sites.

Example 3: Thermostability of cutinase variants

Variants

The thermostability was tested as described below for the *H. insolens* cutinase and the following variants thereof:

A14P+ E47K

E47K

E179Q

E6Q+ E47K+ R51P

A14P+ E47K+ E179Q

E6Q+ A14P+ E47K+ R51P+ E179Q

E6Q+ E10Q+ A14P+ E47K+ R51P+ E179Q

Differential Scanning Calorimetry (DSC)

Thermostability of cutinase variants was investigated by means of DSC at pH 4.5 (50 mM acetate buffer) and pH 8.5 (50mM glycyl-glycine buffer). The thermal denaturation temperature, T_d, was taken as the top of denaturation peak (major endothermic peak) in thermograms (Cp vs. T) obtained after heating of enzyme solutions at a constant programmed heating rate.

The parent cutinase was found to have T_d of 63°C at pH 8.5. Six of the above variants were found to have T_d of 70-73°C, i.e. an improvement of 7-10°.

The parent cutinase was found to have T_d of 61°C at pH 4.5. Five of the above variants were found to have T_d of 64-66°C, i.e. an improvement of 3-5°.

Hydrolysis of BETEB

The thermostability of the *H. insolens* cutinase and two of the above variants was measured by hydrolysis of BETEB at elevated temperature. For each cutinase, the following mixture was incubated for 17 hours at various temperatures in the range 55-70°C:

0.1 ml 0.5 M glycyl-glycine buffer (pH 8.5)

0.1 ml 0.5 % BETEB dissolved in ethanol

0.1 ml enzyme solution (approx. 25 LU/ml)

0.7 ml Milli Q water

The degree of hydrolysis was measured after the incubation. The results are shown in the table below.

	Variant	Variant	Parent
	27 LU/ml	25 LU/ml	24 LU/ml
55°C	98 %	99 %	72 %
60°C	91 %	83 %	33 %
65°C	66 %	13 %	7 %

These results clearly show that the variants have improved thermostability compared to the parent cutinase.

Hydrolysis of BETEB

The thermostability of the *H. insolens* cutinase and three of the above variants was measured by hydrolysis of BETEB at 60°C for 2 hours. The hydrolysis was carried out at the above conditions, except that the temperature was fixed at 60°C and the cutinase dosage was varied. The results below are shown in the table below.

LU/ml	Variant	Variant	Variant	Parent
0	0 %	0 %	0 %	0 %
10	97 %	99 %	9 %	6 %
20	98 %	99 %	74 %	
50	98 %	94 %	93 %	15 %
100	88 %	69 %	92 %	34 %
300				41 %
600				63 %
1200				82 %

The results show a much faster hydrolysis at 60°C with the variants than with the parent cutinase.

Example 4: Hydrolysis of c3ET

The *H. insolens* cutinase and five of the above variants were tested in hydrolysis of c3ET at elevated temperature. For each cutinase, the following mixture was incubated for 2 hours at various temperatures.

0.115mg c3ET (0.1ml of 2mM c3ET dissolved in HFIP was taken in reaction vessel. Solvent was removed under vacuum, then dried up at 70°C over night)

0.1ml 0.5M glycyl-glycine buffer (pH8.5)

0.1ml enzyme solution (approx. 600LU/ml)

0.8ml Milli Q water

After the incubation, 2ml of 1,1,1,3,3,3-Hexafluoro-2-propanol (HFIP) was added to each reaction mixture, then hydrolysis ratio was measured by HPLC. The results shown in Fig 3 clearly indicate that the variants have improved thermostability compared to the parent cutinase.

Example 5: Hydrolysis of c3ET on yarn

The thermostability of the *H. insolens* cutinase five of the above variants was tested using polyester yarn containing c3ET as by product. The following substrate mixture was preincubated at 60 or 65°C:

0.1g polyester yarn

0.2ml 0.5M glycyl-glycine buffer (pH8.5)

1.7ml Milli Q water

After preincubation, 0.1ml enzyme solution (approx. 1000 LU/ml) was added to each reaction vessel and incubated for 17 hours. Then 2ml HFIP was added and left for 30 minutes to extract and hydrolyze c3ET sitting on the surface of the polyester yarn; then the hydrolysis ratio was measured. The results are shown in Fig. 4.

It is seen that the variants are more effective than the parent cutinase for hydrolyzing c3ET on polyester yarn. One variant gives higher hydrolysis ratio at 65°C than at 60°C.

Example 6: Treatment of yarn with cutinase variant

Time courses of c3ET hydrolysis on polyester yarn at different temperature or dosage were examined. Time course at different temperatures is shown in Fig 5. It is seen that the optimum temperature is 65°C. At 70°C there is still about half of the activity left. Time course with increased enzyme dosage is shown in Fig 6. The curves at dosage 275 and 550 LU/ml are seen to be the same, indicating that the hydrolysis ratio reached to plateau between dosage of 100 to 275 LU/ml. Presumably 200LU/ml is enough.

Example 7: Dyeing polyester with reactive dye

The following polyester fabrics were treated:

woven fabric; ca. 2 x 2 cm, 34mg

knitted fabric; ca. 1.5 x 1.5 cm, 50mg

Each fabric was soaked in 0.9 ml, 50 mM GlyGly (glycyl-glycine) buffer (pH 8.5) and 0.1 ml solution of a variant of the *H. insolens* cutinase (1100 LU/ml), and incubated at 65 or 70°C. After one day, another 0.1 ml enzyme solution was added, incubation was continued for two more days, the fabrics were then taken out and rinsed in water. A comparative experiment was made with the parent cutinase, and a blank was treated in the same manner without enzyme.

The fabrics were stirred in a mixture of 9 g 120 g Na_2SO_4 and 60 g Na_2CO_3 in 3 liter deionized water at 60 °C for 30 min, and then rinsed with running warm water. The reactive dye was Celmazol Brilliant Blue B (product of Mitsui Chemical Co., Japan), which has the structure Chromophore-NHPh-$SO_2CH_2CH_2OSO_3Na$.

In all four experiments, (woven and knitted, 65 and 70°C), the fabrics were uniformly dyed.

Example 8: Solubilization of polyester fragments from knitted textile

A 1x1 cm sample of knitted polyester textile (PET, polymer of ethyleneglycol and terephthalic acid) was incubated for 1 hour in 1 ml of buffer at pH 10, 60°C with 0.01 mg of a variant of *H. insolens* cutinase. The reaction mixture was separated, and the release of terephthalic acid was found by measuring OD at 250 nm (ex-

pressed as OD_{250}/mg PET). comparative experiments were made without enzyme or with the parent cutinase. Results:

	Enzyme	OD_{250}
Invention	Cutinase variant	4.5
Reference	Parent cutinase	0.3
	None	0.1

The results show that the variant is effective in solubilizing polyester.

In another experiment, the cutinase variant was tested for 2 hours at 65°C with and without the addition of a non-ionic surfactant (alcohol ethoxylate, product name Softanol 50), using various amounts of the variant from 0.5 to 200 LU/ml. The results showed more solubilization in the presence of non-ionic surfactant.

Example 9: Hydrolysis of polycaprolactone and polyester film

About 0.1 g of polycaprolactone or polyester film were put in tubes. They were soaked in 5ml of 50mM GlyGly buffer (pH 8.5) with or without a variant of *H. insolens* cutinase (450 LU). They were incubated at 70°C for 5 hours. After the reaction we observed a thin layer of hydrolysate on the surface of the tubes with enzyme, both with polycaprolactone and with polyester film. On the other hand no change was observed in controls without enzyme. In the case of polycaprolactone there was 10% of weight loss. We see no weight change of polyester.

Example 10: cPET hydrolysis

The performance of a cutinase variant was compared with the parent enzyme (*H. insolens* cutinase). The trials were done as follows:

An oligomer-stained swatch of (black) PET-fabric (app. 4cm x 13cm) is subjected to the enzyme-treatment at relatively low agitation in a so-called mini-tergitometer apparatus. The PET-fabric is mounted onto a cylindrical, perforated holder (radius ca.2 cm, height ca 6 cm) , that rotates around its axis, and with the oligomer stained side of the PET fabric facing the exterior of the cylinder.

The fabric is immersed in a 150ml glass-beaker containing 100ml of the treatment solution at a given temperature (here 65°C). After a given treatment time

(here 90minutes) the PET swatch is removed from the bath and rinsed in deionized water and air dried.

After conditioning the swatches are visually ranked (with respect to oligomer stain removal) on the side having the oligomer-staining. The rating being as follows:

-2: Sample significantly worse than blank (no enzyme)

-1: Sample slightly worse than blank (no enzyme)

0: Sample can not be distinguished from blank

1: Sample slightly improved vs blank

2: Sample significantly improved over blank

Also, the swatches are read spectrofotometrically (apparatus: Hunterlab Reflectometer) to quantify the color strength (K/S-value at 600nm).

The table below summarizes the test-conditions for a trial comparing the performance the enzymes under similar conditions:

Temperature:	65°C
Buffer/pH:	50 mM glycine buffer, pH 10.3
Treatment time (min)	90
Dosage of Enzyme (LU/g)	30000

Results from the trial are summarized below

Enzyme	Visual rating (avg.)	K/S Difference @ 600 nm
None	0 (defined)	2.33
Parent cutinase	0	2.38
Cutinase variant	1.5-2.0	2.89

From this set of experiments it thus appears that the parent enzyme provides no or only very limited effect at the given test conditions (probably because the temperature is too high for the enzyme to retain activity), while the cutinase variant provides a substantial removal of the oligomer staining from the PET-fabric.

Example 11: cPET hydrolysis

The pH and temperature profile of a variant of *H. insolens* cutinase was tested in a model disperse dyeing experiment. The trials were performed as follows:

An oligomer-stained swatch of (black) PET-fabric is subjected to the conditions of a typical disperse dyeing sequence in a Werner Mathis Labomat. In overview of the process, the swatch is added to a buffer solution, heated to 130°C, cooled down to the treatment temperature. Enzyme or buffer is added and then held at the desired temperature for 30 minutes. The solution is cooled down to room temperature and turbidity in the wash liquor is measured. The reduction in turbidity is a direct measure of the cutinase activity, corresponding to hydrolyzed cPET oligomers.

Detailed description of the experiment:

A black PET (app. 4cm x 13cm) swatch is added 140 ml 100 mM Britton-Robinson buffer containing 0.2 g/l Lutensol AT11 (BASF) and loaded in the Labomat (32 rotation per minute).

The Labomat is heated to 130°C at a gradient of 9°C/minute, and held for 10 minutes.

The beakers are cooled to run temperature (according to table below) at a gradient of 9°C/minute, and held for 1 minute.

10 mL enzyme solution (100 LU/ml of the variant) or buffer solution (0 LU/ml) at appropriate pH is injected to the beakers.

The Labomat is re-heated to temperature at a gradient of 2°C/minute, and held for 30 minutes.

The swatches are removed, and the wash liquor is cooled down to room temperature.

Turbidity of the wash liquors are measured.

Evaluation: Turbidity is measured on Hach 18900 Ratio Turbidimeter (standardized with 1.8, 18, and 180 NTU Turbidity Standards). Enzyme performance is calculated relative to a blank as the difference between turbidity of blank liquor (no enzyme) and turbidity of enzyme treated liquor.

The relative performance (reduction in turbidity) of the cutinase variant is calculated, and the results are shown in the following table. When a negative num-

ber is obtained, then the result is given as "negative". A negative number is assumed to be an artifact, caused by the variation of the set up.

Temperature	pH 7	pH 8	pH 9	pH 10
60°C	39	57	37	14
65°C	39	16	60	30
70°C	25	12	54	33
75°C	22	50	114	58
85°C	negative	negative	15	negative

The results show that the cutinase variant is active over a broad pH and temperature range, with optimum oligomer removal in the current set up around pH 9 and 75°C. Inactivation seems to occur at or above 85°C.

Example 12: cPET hydrolysis

The effect of treatment time was investigated for a variant of *H. insolens* cutinase in a model disperse dyeing experiment. The trials were performed as follows:

An oligomer-stained swatch of (black) PET-fabric is subjected to the conditions of a typical disperse dyeing sequence in a Werner Mathis Labomat. In overview of the process, the swatch is added to a buffer solution, heated to 130°C, cooled down to the treatment temperature. Enzyme or buffer (100 mM Britton-Robinson pH 9) is added, and then held at 75°C for 0-40 minutes. The solution is cooled down to room temperature and turbidity in the wash liquor is measured. The reduction in turbidity is a direct measure of the cutinase activity, corresponding to hydrolyzed cPET oligomers.

Detailed description of the experiment:

A black PET (app. 4cm x 13cm) swatch is added to 140 ml 100 mM Britton-Robinson buffer containing 0.2 g/l Lutensol AT11 (BASF) and loaded in the Labomat (32 rotation per minute).

The Labomat is heated to 130°C at a gradient of 9°C/minute, and the temperature is held for 10 minutes.

The beakers are cooled to 75°C at a gradient of 9°C/minute, and held for 1 minute.

10 mL enzyme solution (100 LU/ml of variant) or 100 mM Britton-Robinson buffer pH 9.0 (0 LU/ml) is injected into the beakers.

The Labomat is re-heated to 75°C at a gradient of 2°C/minute, and held for the appropriate number of minutes (0-40 minutes, see table below).

The swatches are removed, and the wash liquor is cooled down to room temperature.

Turbidity of the wash liquors are measured.

Evaluation: Turbidity is measured on Hach 18900 Ratio Turbidimeter (standardized with 1.8, 18, and 180 NTU Turbidity Standards). Enzyme performance is calculated relative to a blank at time equal to zero: Turbidity of blank liquor at time zero (no enzyme) subtracted turbidity of enzyme treated liquor (at a given time).

The relative performance (reduction in turbidity) of the cutinase variant was calculated, and the results are shown in the following table.

Time (minutes)	Relative performance (Reduction in turbidity)
0	0
5	42
10	48
15	62
20	69
25	85
30	72
40	78

The results show that the effect of the enzyme is increased over time. At the current enzyme dose and oligomer concentration, it seems to level off above approx. 20 minutes.

Example 13: Fiber modification

The effect on wetting characteristics of a disperse dyed polyester fabric was investigated by treating the fabric with a variant of *H. insolens* cutinase prior to dye-

ing. The experiment therefore consisted of two phases, the actual fiber modification and the disperse dyeing pro- cedure.

Phase 1 - Fiber Modification:

Equipment:	Atlas Launder-O-meter LP2
Fabric:	knit 100 % scoured polyester from Testfabrics
pH:	50 mM potassium phosphate buffer, pH 7
Abrasives:	5 big steel balls
Beaker Vol.:	120 mL
Treatment:	2 hours 65°C then ramped up to 90°C and held for 1 hour
Swatch Prep:	Cut 3* 1.5 g swatch of fabric, 3 per beaker = 4.5 g

Rinse:

Rinse in deionized water.

Phase 2 - Dyeing - disperse dye:

Dye Solution:

Add together with deionized water to make liquor ratio 1:20-

0.4 % Dianix Red (DyStar) SE-CB (owf)

pH to 4.5 - 5

Dyeing Procedure:

1. One swatch per treatment from the fiber modification is used for the dyeing (1.5 g/swatch is used for the liquor ratio calculation).

2. Make dyebath according to the recipe above. Add the cold dye solution to the Labomat beakers and heat to 55°C at a gradient of 3.5°C/minute. Run for 5 minutes once temperature has been reached.

3. Add the fabric to the beaker.

4. Raise temperature to 130°C at a gradient of 1.5°C/minute. Dye for 30 minutes.

5. Cool to 70°C at a gradient of 5°C/minute. Drop bath, but collect, and rinse fabric hot (60°C) for 10 minutes. Follow the hot rinse with a room temperature overflow rinse until all bleeding had stopped.

6. Let air dry overnight.

Tests/Analysis:

AATCC Test Method 61 - Colorfastness to washing

Percent Dyebath Exhaustion - Spectrophotometer

K/S and L* - Reflectometer

AATCC TM-79 Drop Test

Results:

The results from the fiber modification are shown in the following table.

Variant dosage	Staining (AATCC TM-61)	Color Change (K/S @ 530 before and after TM-61)	Drop Test (AATCC TM-79)
Blank	4.5	5	53 sec.
50 LU/mL	4.5	5	18 sec.
100 LU/mL	4.5	5	15 sec.

The results show that the treatment of polyester with the variant increases the wetting substantially. No adverse effects are noticed on the dyeability with the disperse dye in the current set-up.

Example 14: Malodor reduction in textiles soiled with human sweat/sebum by use of a cutinase variant in laundry

The performance of cutinase, with respect to malodor reduction, can be tested in a one-cycle washing trial carried out in a Terg-O-tometer.

Experimental conditions:

Washing liquor: 1000 ml per beaker

Swatches: 100 % polyester (interlock knitted, previously cleaned by Soxhlet extraction). 24 swatches (3.3 × 3.5 cm) per beaker.

Soil: Human male axillary sweat and sebum applied by wiping the armpits after exercise.

Detergent: 5 g/L of a standard color detergent. No pH adjustment.

Water hardness: 3.2 mM Ca^{2+}/Mg^{2+} (in a ratio of 5:1)

Wash Temperature: 30°C

Wash time: 30 min

Rinse: 15 minutes in running tap water

Evaluation:

After wash the wet swatches are placed in closed, tinted 200 ml glasses. A trained sensory panel (9-11 judges) evaluates the odor by sniffing the headspace over the wet samples and evaluates the total odor intensity. The odor intensity is noted by placing a mark on an unstructured line scale measuring 15 cm, with word anchors at each end ('nothing' at the beginning of the scale and 'very strong' at the end). All evaluations are performed twice. The swatches are evaluated on day 1, 2 and 3 after wash (swatches are kept in the glasses at all times).

CLAIMS

1. A variant of a parent fungal cutinase, which variant:

a) comprises substitution of one or more amino acid residues at a position which is located:

i) within 17 Å from the location of the N-terminal amino acid (as calculated from amino acid residues in a crystal structure), and/or

ii) within 20 positions from the N-terminal amino acid, and

b) is more thermostable than the parent cutinase.

2. The variant of the preceding claim which comprises substitution of one or more amino acid residues at a position which is located:

i) within 12 Å from the location of the N-terminal amino acid (as calculated from amino acid residues in a crystal structure), and/or

ii) within 15 positions from the N-terminal amino acid.

3. A variant of a parent fungal cutinase comprising substitution of one or more amino acid residues which is located:

a) within 17 Å from the location of the N-terminal amino acid (as calculated from amino acid residues in a crystal structure), and/or

b) within 20 positions from the N-terminal amino acid,

with the proviso that it is not a variant of the cutinase of *Fusarium solani pisi* having one of the substitutions R17, T18, T19V, D21N, I24E, Y38F, R40, G41A, S42, T43, E44, T45, G46, N47R, G49, T50, L51, P53, S54, A56C, S57, N58R, S61, A62E, K65A, D66S, G67D, W69Y, I70C, G74, G75, R78, Y119, G192, P193, D194R, A195, R196, G197V, or A199C (*Fusarium solani pisi* cutinase numbering).

4. A variant of a parent fungal cutinase comprising substitution of one or more amino acid residues which:

a) has a solvent accessible surface, and

b) is located:

i) within 17 Å from the location of the N-terminal amino acid (as calculated from amino acid residues in a crystal structure), and/or

ii) within 20 positions from the N-terminal amino acid,

with the proviso that it is not a variant of the cutinase of *Fusarium solani pisi* having one of the substitutions T18, Y38F, R40, G41A, S42, T43, E44, T45, N47R, G49, T50, L51, P53, S54, A56C, A62E or G192 (*Fusarium solani pisi* cutinase numbering).

5. A variant of a parent fungal cutinase comprising substitution of one or more amino acid residues which is located:

a) less than 12 Å from the location of the N-terminal amino group (as calculated from amino acid residues in a crystal structure), and/or

b) within 15 positions from the N-terminal amino acid,

with the proviso that the variant is not the cutinase of *Fusarium solani pisi* having one of the substitutions R17, T18, T19V, D21N, Y38F, R40, T45, G46, N47R, G49, T50, L51, P53, S54, A56C, S57, N58R, K65A or I70C (*Fusarium solani pisi* cutinase numbering).

6. The variant of any preceding claim wherein the parent cutinase is native to a filamentous fungus, preferably a strain of *Humicola* or *Fusarium*, preferably *H. insolens* or *F. solani pisi*, most preferably *H. insolens* strain DSM 1800.

7. The variant of any preceding claim wherein the parent cutinase has an amino acid sequence which can be aligned with the cutinase of *H. insolens* strain DSM 1800.

8. The variant of any preceding claim wherein the parent cutinase has an amino acid sequence which is at least 50 % homologous to the cutinase of *H. insolens* strain DSM 1800, preferably at least 70 % homologous, more preferably at least 80 % homologous.

9. A variant of a parent fungal cutinase from *Humicola insolens* which comprises substitution of one or more amino acid residues located:

a) within 17 Å from the location of the N-terminal amino acid (as calculated from amino acid residues in a crystal structure), and/or

b) within 20 positions from the N-terminal amino acid.

10. The variant of the preceding claim which comprises substitution of one or more amino acid residues located:

a) less than 12 Å from the location of the N-terminal amino group (as calculated from amino acid residues in a crystal structure), and/or

b) within 15 positions from the N-terminal amino acid

11. The variant of any preceding claim which comprises substitution of one or more amino acids having a solvent accessible surface.

12. The variant of any preceding claim wherein one or more substitutions is substitution of a negatively charged amino acid with a neutral or positively charged amino acid or substitution of a neutral amino acid with a positively charged amino acid.

13. The variant of the preceding claim wherein one or more substitutions is at a position corresponding to position E6, E10, E30, E47, D63, E82 and/or E179 in the cutinase of *Humicola insolens* strain DSM 1800, preferably a substitution with R/K/Y/H/Q/N, more preferably a substitution corresponding to E6N/Q, E10N/Q, E47K/R and/or E179N/Q (*H. insolens* cutinase numbering).

14. The variant of any preceding claim wherein one or more substitutions is substitution with a Pro residue, preferably at a position corresponding to position A14 and/or R51.

15. The variant of any preceding claim which has one, two, three, four, five or six of said substitutions.

16. The variant of any preceding claim which has substitutions corresponding to one of the following in the cutinase of *Humicola insolens* strain DSM 1800:

a) R51P
b) E6N/Q + L138I
c) A14P + E47K
d) E47K
e) E179N/Q
f) E6N/Q + E47K + R51P
g) A14P + E47K + E179N/Q
h) E47K + E179N/Q
i) E47K + D63N
j) E6N/Q + A14P + E47K + R51P + E179N/Q
k) E6N/Q + E10N/Q + A14P + E47K + R51P + E179N/Q, or
l) Q1P + L2V + S11C + N15T + F24Y + L46I + E47K

17. The variant of any preceding claim which has hydrolytic activity towards terephthalic acid esters, particularly towards cyclic tri(ethylene terephthalate) and/or Terephthalic acid bis(2-hydroxyethyl)ester dibenzoate (BETEB).

18. The variant of any preceding claim which has a denaturation temperature which is at least 5° higher than the parent cutinase, preferably measured at pH 8.5

19. A DNA sequence encoding the variant of any preceding claim.

20. A vector comprising the DNA sequence of the preceding claim.

21. A transformed host cell harboring the DNA sequence of claim 19 or the vector of claim 20.

22. A method of producing the variant of any of claims 1-18 comprising

a) cultivating the cell of claim 21 so as to express and preferably secrete the variant, and

b) recovering the variant.

23. A method of constructing a cutinase variant, which method comprises:

a) selecting a parent fungal cutinase,

b) identifying one or more amino acid residues in the parent cutinase at positions which are:

i) within 17 Å from the location of the N-terminal amino acid (as calculated from amino acid residues in a crystal structure), and/or

ii) within 20 positions from the N-terminal amino acid, and

c) making alterations each of which is an insertion, a deletion or a substitution of the amino acid residue,

d) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b),

e) preparing the variant resulting from steps b-d,

f) testing the thermostability of the variant,

g) optionally repeating steps b-f, and

h) selecting a variant having higher thermostability than the parent cutinase.

24. A method of producing a cutinase variant, which method comprises:

a) selecting a parent fungal cutinase,

b) identifying one or more amino acid residues in the parent cutinase at positions which are:

i) within 17 Å from the location of the N-terminal amino acid (as calculated from amino acid residues in a crystal structure), and/or

ii) within 20 positions from the N-terminal amino acid, and

c) making alterations each of which is an insertion, a deletion or a substitution of the amino acid residue,

d) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b),

e) preparing the variant resulting from steps b-d,

f) testing the thermostability of the variant,

g) optionally repeating steps b-f,

h) selecting a variant having higher thermostability than the parent cutinase, and

i) producing the variant to obtain the cutinase variant.

25. A process for enzymatic hydrolysis of a cyclic oligomer of poly(ethylene terephthalate), which process comprises treating the cyclic oligomer with a variant of a parent fungal cutinase, which variant comprises substitution of one or more amino acid residues at a position which is located:

i) within 17 Å from the location of the N-terminal amino acid (as calculated from amino acid residues in a crystal structure), and/or

ii) within 20 positions from the N-terminal amino acid.

26. The process of the preceding claim, in which the cyclic oligomer is cyclic tri(ethylene terephthalate).

27. The process of claim 25 or 26 wherein the treatment is done at 60-80°C, preferably at 65-75°C.

28. The process of any of claims 25-27 wherein the cyclic oligomer is present in and on the fibers of a polyester containing fabric or yarn.

29. The process of any of claims 25-28 which further comprises subsequently rinsing the fabric or yarn, preferably rinsing with an aqueous solution having a pH in the range of from about pH 7 to about pH 11.

30. A process for dyeing polyester fabric or yarn, comprising:

a) treating the fabric or yarn with a cutinase having a thermal denaturation temperature of 65°C or higher at pH 8.5; and

b) dyeing the treated fabric with a reactive dye or a disperse dye.

31. The process of the preceding claim wherein the cutinase is the variant of any of claims 1-18.

32. A detergent composition comprising a surfactant and the variant of any of claims 1-18.

33. A method for detecting cutinase activity in a sample, comprising incubating the sample with terephthalic acid bis(2-hydroxyethyl)ester dibenzoate and detecting hydrolysis of said ester.

34. A process for improving the functional finish of a PET-containing yarn or fabric comprising

a) treating the yarn or fabric with the variant of any of claims 1-18, and

b) subsequently the yarn or fabric with a finishing agent selected from the group consisting of softeners, anti-crease resins, anti-static agents, anti-soiling agents.

Fig. 1

3D structure of cutinase from *Humicola insolens*

ATOM	1	N	GLY	A	3	24.424	-7.935	18.390	1.00 46.73
ATOM	2	CA	GLY	A	3	23.848	-8.994	17.546	1.00 42.29
ATOM	3	C	GLY	A	3	24.396	-10.112	16.727	1.00 37.35
ATOM	4	O	GLY	A	3	25.347	-10.913	16.728	1.00 35.38
ATOM	5	N	ALA	A	4	23.664	-10.625	15.797	1.00 34.53
ATOM	6	CA	ALA	A	4	23.051	-10.874	14.555	1.00 30.95
ATOM	7	C	ALA	A	4	21.574	-11.246	14.920	1.00 28.33
ATOM	8	O	ALA	A	4	20.677	-10.499	14.446	1.00 22.94
ATOM	9	CB	ALA	A	4	23.574	-11.780	13.556	1.00 26.92
ATOM	10	N	ILE	A	5	21.583	-12.058	16.043	1.00 26.48
ATOM	11	CA	ILE	A	5	20.281	-12.289	16.637	1.00 25.65
ATOM	12	C	ILE	A	5	20.316	-12.151	18.118	1.00 22.40
ATOM	13	O	ILE	A	5	21.060	-12.888	18.717	1.00 24.74
ATOM	14	CB	ILE	A	5	19.724	-13.683	16.524	1.00 26.04
ATOM	15	CG1	ILE	A	5	19.852	-13.927	15.050	1.00 29.85
ATOM	16	CG2	ILE	A	5	18.374	-13.558	17.159	1.00 20.48
ATOM	17	CD1	ILE	A	5	19.066	-15.133	14.709	1.00 27.96
ATOM	18	N	GLU	A	6	19.461	-11.377	18.668	1.00 20.52
ATOM	19	CA	GLU	A	6	19.207	-11.015	20.040	1.00 17.94
ATOM	20	C	GLU	A	6	17.711	-11.027	20.432	1.00 17.76
ATOM	21	O	GLU	A	6	16.931	-10.165	19.990	1.00 17.60
ATOM	22	CB	GLU	A	6	19.809	-9.614	20.199	1.00 14.22
ATOM	23	CG	GLU	A	6	21.232	-9.374	20.385	1.00 16.71
ATOM	24	CD	GLU	A	6	22.148	-10.387	21.030	1.00 34.47
ATOM	25	OE1	GLU	A	6	21.634	-11.347	21.693	1.00 49.57
ATOM	26	OE2	GLU	A	6	23.410	-10.310	20.975	1.00 37.43
ATOM	27	N	ASN	A	7	17.375	-11.895	21.333	1.00 21.67
ATOM	28	CA	ASN	A	7	16.070	-11.854	21.846	1.00 24.04
ATOM	29	C	ASN	A	7	15.927	-11.488	23.238	1.00 22.08
ATOM	30	O	ASN	A	7	15.098	-12.179	23.820	1.00 24.00
ATOM	31	CB	ASN	A	7	15.468	-13.307	21.820	1.00 25.06
ATOM	32	CG	ASN	A	7	15.039	-13.160	20.341	1.00 38.52
ATOM	33	OD1	ASN	A	7	15.519	-14.147	19.759	1.00 48.45
ATOM	34	ND2	ASN	A	7	14.318	-12.081	19.968	1.00 36.89
ATOM	35	N	GLY	A	8	16.671	-10.813	23.926	1.00 23.56
ATOM	36	CA	GLY	A	8	16.654	-10.628	25.363	1.00 23.69
ATOM	37	C	GLY	A	8	15.366	-10.247	25.984	1.00 22.72
ATOM	38	O	GLY	A	8	14.967	-10.939	26.867	1.00 32.25
ATOM	39	N	LEU	A	9	14.785	-9.144	25.755	1.00 23.61
ATOM	40	CA	LEU	A	9	13.470	-8.753	26.033	1.00 23.73
ATOM	41	C	LEU	A	9	12.559	-9.961	25.782	1.00 25.93
ATOM	42	O	LEU	A	9	11.494	-10.054	26.480	1.00 30.47
ATOM	43	CB	LEU	A	9	12.971	-7.621	25.105	1.00 5.84
ATOM	44	CG	LEU	A	9	11.556	-7.227	25.470	1.00 23.25
ATOM	45	CD1	LEU	A	9	11.422	-6.765	26.968	1.00 20.21
ATOM	46	CD2	LEU	A	9	11.009	-6.071	24.714	1.00 17.64
ATOM	47	N	GLU	A	10	12.775	-10.786	24.773	1.00 29.56

ATOM	48	CA	GLU	A	10	11.635	-11.681	24.484	1.00	33.93
ATOM	49	C	GLU	A	10	11.640	-12.872	25.412	1.00	32.18
ATOM	50	O	GLU	A	10	10.600	-13.159	25.996	1.00	36.67
ATOM	51	CB	GLU	A	10	11.513	-11.996	23.012	1.00	40.97
ATOM	52	CG	GLU	A	10	10.054	-12.303	22.745	1.00	51.96
ATOM	53	CD	GLU	A	10	9.570	-11.711	21.437	1.00	54.08
ATOM	54	OE1	GLU	A	10	10.488	-11.440	20.635	1.00	48.22
ATOM	55	OE2	GLU	A	10	8.323	-11.643	21.471	1.00	52.39
ATOM	56	N	SER	A	11	12.822	-13.334	25.688	1.00	29.58
ATOM	57	CA	SER	A	11	12.993	-14.455	26.645	1.00	35.25
ATOM	58	C	SER	A	11	13.403	-14.012	28.047	1.00	39.86
ATOM	59	O	SER	A	11	13.688	-14.790	28.919	1.00	43.72
ATOM	60	CB	SER	A	11	14.053	-15.364	25.983	1.00	33.73
ATOM	61	OG	SER	A	11	15.275	-14.620	25.928	1.00	46.98
ATOM	62	N	GLY	A	12	13.467	-12.802	28.456	1.00	41.40
ATOM	63	CA	GLY	A	12	13.841	-12.332	29.752	1.00	45.34
ATOM	64	C	GLY	A	12	12.673	-12.562	30.694	1.00	47.62
ATOM	65	O	GLY	A	12	11.485	-12.335	30.335	1.00	50.76
ATOM	66	N	SER	A	13	12.969	-12.900	31.936	1.00	48.09
ATOM	67	CA	SER	A	13	11.974	-13.158	32.995	1.00	45.26
ATOM	68	C	SER	A	13	11.509	-11.933	33.772	1.00	39.53
ATOM	69	O	SER	A	13	12.563	-11.204	33.992	1.00	36.30
ATOM	70	CB	SER	A	13	12.708	-14.006	34.101	1.00	51.20
ATOM	71	OG	SER	A	13	12.006	-13.947	35.338	1.00	57.14
ATOM	72	N	ALA	A	14	10.256	-11.785	34.214	1.00	35.22
ATOM	73	CA	ALA	A	14	10.068	-10.530	34.964	1.00	34.78
ATOM	74	C	ALA	A	14	10.574	-10.620	36.417	1.00	37.51
ATOM	75	O	ALA	A	14	10.809	-9.584	37.113	1.00	38.41
ATOM	76	CB	ALA	A	14	8.714	-9.915	34.903	1.00	32.71
ATOM	77	N	ASN	A	15	11.039	-11.834	36.737	1.00	38.85
ATOM	78	CA	ASN	A	15	11.715	-12.086	37.963	1.00	43.49
ATOM	79	C	ASN	A	15	13.073	-11.411	37.953	1.00	46.45
ATOM	80	O	ASN	A	15	13.453	-11.022	39.022	1.00	52.50
ATOM	81	CB	ASN	A	15	12.088	-13.533	38.207	1.00	53.08
ATOM	82	CG	ASN	A	15	10.772	-14.226	38.553	1.00	71.86
ATOM	83	OD1	ASN	A	15	9.837	-13.535	38.998	1.00	71.73
ATOM	84	ND2	ASN	A	15	10.866	-15.523	38.267	1.00	77.71
ATOM	85	N	ALA	A	16	13.712	-11.305	36.812	1.00	46.73
ATOM	86	CA	ALA	A	16	14.915	-10.470	36.743	1.00	41.22
ATOM	87	C	ALA	A	16	15.031	-9.286	35.798	1.00	36.70
ATOM	88	O	ALA	A	16	16.027	-9.254	35.075	1.00	37.67
ATOM	89	CB	ALA	A	16	15.903	-11.545	36.301	1.00	41.80
ATOM	90	N	CYS	A	17	14.300	-8.227	35.843	1.00	30.62
ATOM	91	CA	CYS	A	17	14.614	-7.093	34.997	1.00	31.78
ATOM	92	C	CYS	A	17	16.024	-6.579	35.149	1.00	32.94
ATOM	93	O	CYS	A	17	16.744	-6.850	36.113	1.00	39.10
ATOM	94	CB	CYS	A	17	13.679	-5.881	35.138	1.00	28.00
ATOM	95	SG	CYS	A	17	12.048	-6.583	34.858	1.00	24.72

ATOM	96	N	PRO	A	18	16.529	-5.910	34.092	1.00	30.49
ATOM	97	CA	PRO	A	18	17.994	-5.626	33.971	1.00	22.04
ATOM	98	C	PRO	A	18	18.178	-4.138	34.241	1.00	20.15
ATOM	99	O	PRO	A	18	17.085	-3.459	34.370	1.00	17.83
ATOM	100	CB	PRO	A	18	18.353	-6.003	32.559	1.00	19.20
ATOM	101	CG	PRO	A	18	17.044	-6.595	32.101	1.00	20.16
ATOM	102	CD	PRO	A	18	15.903	-5.936	32.792	1.00	24.35
ATOM	103	N	ASP	A	19	19.428	-3.652	34.011	1.00	14.85
ATOM	104	CA	ASP	A	19	19.451	-2.168	34.226	1.00	16.59
ATOM	105	C	ASP	A	19	18.739	-1.367	33.156	1.00	20.42
ATOM	106	O	ASP	A	19	18.311	-0.242	33.430	1.00	23.84
ATOM	107	CB	ASP	A	19	20.896	-1.818	34.485	1.00	27.25
ATOM	108	CG	ASP	A	19	21.433	-2.389	35.793	1.00	42.30
ATOM	109	OD1	ASP	A	19	21.162	-3.549	36.297	1.00	53.52
ATOM	110	OD2	ASP	A	19	22.251	-1.719	36.543	1.00	54.02
ATOM	111	N	ALA	A	20	18.646	-1.780	31.895	1.00	20.18
ATOM	112	CA	ALA	A	20	18.066	-1.036	30.809	1.00	17.43
ATOM	113	C	ALA	A	20	17.713	-2.087	29.703	1.00	16.06
ATOM	114	O	ALA	A	20	18.334	-3.172	29.860	1.00	9.45
ATOM	115	CB	ALA	A	20	18.975	-0.048	30.100	1.00	12.07
ATOM	116	N	ILE	A	21	16.814	-1.602	28.829	1.00	8.47
ATOM	117	CA	ILE	A	21	16.657	-2.583	27.753	1.00	9.23
ATOM	118	C	ILE	A	21	16.952	-1.745	26.486	1.00	14.77
ATOM	119	O	ILE	A	21	16.681	-0.473	26.403	1.00	12.01
ATOM	120	CB	ILE	A	21	15.208	-2.984	27.837	1.00	16.28
ATOM	121	CG1	ILE	A	21	14.851	-3.898	28.956	1.00	15.55
ATOM	122	CG2	ILE	A	21	14.689	-3.671	26.514	1.00	13.71
ATOM	123	CD1	ILE	A	21	13.401	-3.879	29.372	1.00	6.12
ATOM	124	N	LEU	A	22	17.432	-2.451	25.391	1.00	12.24
ATOM	125	CA	LEU	A	22	17.665	-1.774	24.087	1.00	11.27
ATOM	126	C	LEU	A	22	16.849	-2.517	23.038	1.00	14.60
ATOM	127	O	LEU	A	22	16.908	-3.781	22.850	1.00	9.78
ATOM	128	CB	LEU	A	22	19.087	-1.865	23.693	1.00	10.96
ATOM	129	CG	LEU	A	22	19.493	-1.543	22.257	1.00	10.32
ATOM	130	CD1	LEU	A	22	19.311	-0.081	21.900	1.00	4.72
ATOM	131	CD2	LEU	A	22	20.990	-1.842	22.156	1.00	7.42
ATOM	132	N	ILE	A	23	16.038	-1.815	22.242	1.00	15.13
ATOM	133	CA	ILE	A	23	15.298	-2.459	21.115	1.00	18.06
ATOM	134	C	ILE	A	23	15.916	-1.771	19.901	1.00	17.42
ATOM	135	O	ILE	A	23	16.117	-0.519	19.795	1.00	19.31
ATOM	136	CB	ILE	A	23	13.820	-2.194	21.392	1.00	18.16
ATOM	137	CG1	ILE	A	23	13.208	-3.076	22.447	1.00	14.23
ATOM	138	CG2	ILE	A	23	12.787	-2.167	20.247	1.00	13.19
ATOM	139	CD1	ILE	A	23	12.142	-2.065	22.976	1.00	20.41
ATOM	140	N	PHE	A	24	16.218	-2.548	18.940	1.00	14.59
ATOM	141	CA	PHE	A	24	16.859	-2.159	17.671	1.00	11.72
ATOM	142	C	PHE	A	24	16.347	-2.719	16.353	1.00	7.25
ATOM	143	O	PHE	A	24	16.095	-3.998	16.161	1.00	3.47

ATOM	144	CB	PHE	A	24	18.195	-2.855	17.658	1.00	12.61
ATOM	145	CG	PHE	A	24	19.015	-2.150	16.716	1.00	10.72
ATOM	146	CD1	PHE	A	24	19.457	-0.844	16.913	1.00	13.08
ATOM	147	CD2	PHE	A	24	19.325	-2.852	15.558	1.00	6.61
ATOM	148	CE1	PHE	A	24	20.232	-0.187	15.983	1.00	4.86
ATOM	149	CE2	PHE	A	24	20.061	-2.218	14.545	1.00	7.61
ATOM	150	CZ	PHE	A	24	20.550	-0.823	14.804	1.00	8.78
ATOM	151	N	ALA	A	25	16.037	-1.700	15.449	1.00	6.32
ATOM	152	CA	ALA	A	25	15.662	-2.158	14.068	1.00	7.18
ATOM	153	C	ALA	A	25	16.851	-1.976	13.055	1.00	8.59
ATOM	154	O	ALA	A	25	17.518	-1.000	13.133	1.00	5.95
ATOM	155	CB	ALA	A	25	14.488	-1.402	13.562	1.00	8.27
ATOM	156	N	ARG	A	26	17.174	-3.032	12.325	1.00	8.84
ATOM	157	CA	ARG	A	26	18.134	-3.278	11.277	1.00	4.04
ATOM	158	C	ARG	A	26	17.691	-2.694	9.894	1.00	7.67
ATOM	159	O	ARG	A	26	16.527	-2.361	9.525	1.00	9.36
ATOM	160	CB	ARG	A	26	18.581	-4.659	10.756	1.00	6.06
ATOM	161	CG	ARG	A	26	17.705	-5.741	10.439	1.00	5.08
ATOM	162	CD	ARG	A	26	18.069	-7.224	10.382	1.00	6.73
ATOM	163	NE	ARG	A	26	17.000	-8.053	9.708	1.00	9.04
ATOM	164	CZ	ARG	A	26	15.724	-8.206	9.912	1.00	7.06
ATOM	165	NH1	ARG	A	26	15.085	-7.535	10.895	1.00	22.93
ATOM	166	NH2	ARG	A	26	14.809	-8.825	9.346	1.00	7.89
ATOM	167	N	GLY	A	27	18.761	-2.539	9.092	1.00	7.71
ATOM	168	CA	GLY	A	27	18.537	-1.888	7.782	1.00	5.34
ATOM	169	C	GLY	A	27	18.063	-2.896	6.862	1.00	4.70
ATOM	170	O	GLY	A	27	18.155	-4.139	7.075	1.00	13.14
ATOM	171	N	SER	A	28	17.562	-2.612	5.765	1.00	11.82
ATOM	172	CA	SER	A	28	17.108	-3.325	4.615	1.00	14.72
ATOM	173	C	SER	A	28	18.214	-4.327	4.142	1.00	7.74
ATOM	174	O	SER	A	28	19.286	-3.973	4.083	1.00	6.71
ATOM	175	CB	SER	A	28	16.460	-2.352	3.538	1.00	6.38
ATOM	176	OG	SER	A	28	16.819	-0.978	3.833	1.00	28.10
ATOM	177	N	THR	A	29	17.942	-5.634	4.241	1.00	4.79
ATOM	178	CA	THR	A	29	18.562	-6.763	3.914	1.00	8.71
ATOM	179	C	THR	A	29	19.500	-7.271	4.985	1.00	14.00
ATOM	180	O	THR	A	29	20.162	-8.326	4.713	1.00	17.68
ATOM	181	CB	THR	A	29	19.454	-6.680	2.617	1.00	14.90
ATOM	182	OG1	THR	A	29	20.736	-6.066	2.595	1.00	14.00
ATOM	183	CG2	THR	A	29	18.785	-5.888	1.561	1.00	15.59
ATOM	184	N	GLU	A	30	19.740	-6.599	6.105	1.00	14.52
ATOM	185	CA	GLU	A	30	20.677	-7.266	7.056	1.00	14.10
ATOM	186	C	GLU	A	30	20.092	-8.513	7.647	1.00	13.07
ATOM	187	O	GLU	A	30	18.916	-8.726	7.705	1.00	19.98
ATOM	188	CB	GLU	A	30	21.228	-6.371	8.072	1.00	15.45
ATOM	189	CG	GLU	A	30	21.166	-4.945	7.709	1.00	8.37
ATOM	190	CD	GLU	A	30	22.073	-4.143	8.637	1.00	23.08
ATOM	191	OE1	GLU	A	30	21.395	-3.328	9.284	1.00	19.26

ATOM	192	OE2	GLU	A	30	23.317	-4.327	8.712	1.00	19.71
ATOM	193	N	PRO	A	31	20.875	-9.479	7.918	1.00	13.09
ATOM	194	CA	PRO	A	31	20.477	-10.818	8.402	1.00	14.56
ATOM	195	C	PRO	A	31	20.167	-10.698	9.895	1.00	18.27
ATOM	196	O	PRO	A	31	20.148	-9.636	10.392	1.00	20.45
ATOM	197	CB	PRO	A	31	21.690	-11.692	8.215	1.00	10.95
ATOM	198	CG	PRO	A	31	22.790	-10.664	8.455	1.00	11.24
ATOM	199	CD	PRO	A	31	22.350	-9.316	7.864	1.00	13.71
ATOM	200	N	GLY	A	32	19.612	-11.689	10.472	1.00	18.99
ATOM	201	CA	GLY	A	32	19.205	-11.774	11.816	1.00	13.53
ATOM	202	C	GLY	A	32	18.133	-10.808	12.188	1.00	16.62
ATOM	203	O	GLY	A	32	17.345	-10.294	11.411	1.00	17.01
ATOM	204	N	ASN	A	33	18.055	-10.528	13.468	1.00	16.15
ATOM	205	CA	ASN	A	33	17.290	-9.346	13.823	1.00	14.74
ATOM	206	C	ASN	A	33	18.294	-8.273	14.230	1.00	15.46
ATOM	207	O	ASN	A	33	17.774	-7.184	14.575	1.00	15.90
ATOM	208	CB	ASN	A	33	16.241	-9.663	14.867	1.00	17.42
ATOM	209	CG	ASN	A	33	16.827	-10.201	16.127	1.00	17.97
ATOM	210	OD1	ASN	A	33	16.112	-10.395	17.089	1.00	19.05
ATOM	211	ND2	ASN	A	33	18.074	-10.460	16.112	1.00	13.29
ATOM	212	N	MET	A	34	19.633	-8.378	14.282	1.00	14.22
ATOM	213	CA	MET	A	34	20.282	-7.171	14.751	1.00	12.97
ATOM	214	C	MET	A	34	21.142	-6.663	13.611	1.00	19.02
ATOM	215	O	MET	A	34	21.654	-5.512	13.713	1.00	26.04
ATOM	216	CB	MET	A	34	21.202	-7.329	15.859	1.00	13.39
ATOM	217	CG	MET	A	34	20.579	-7.713	17.163	1.00	9.02
ATOM	218	SD	MET	A	34	20.175	-6.316	18.069	1.00	9.13
ATOM	219	CE	MET	A	34	21.481	-5.121	18.095	1.00	4.11
ATOM	220	N	GLY	A	35	21.259	-7.446	12.550	1.00	19.99
ATOM	221	CA	GLY	A	35	22.071	-7.135	11.418	1.00	14.30
ATOM	222	C	GLY	A	35	23.511	-7.340	11.764	1.00	17.58
ATOM	223	O	GLY	A	35	23.965	-7.724	12.842	1.00	12.78
ATOM	224	N	ILE	A	36	24.450	-6.839	10.950	1.00	20.63
ATOM	225	CA	ILE	A	36	25.833	-7.029	11.277	1.00	17.71
ATOM	226	C	ILE	A	36	26.609	-5.714	11.280	1.00	16.15
ATOM	227	O	ILE	A	36	27.865	-5.618	11.662	1.00	20.30
ATOM	228	CB	ILE	A	36	26.412	-8.070	10.327	1.00	30.19
ATOM	229	CG1	ILE	A	36	26.088	-7.448	8.959	1.00	31.16
ATOM	230	CG2	ILE	A	36	25.944	-9.490	10.543	1.00	15.68
ATOM	231	CD1	ILE	A	36	26.922	-8.149	7.958	1.00	34.10
ATOM	232	N	THR	A	37	25.905	-4.589	11.040	1.00	13.00
ATOM	233	CA	THR	A	37	26.825	-3.396	11.141	1.00	9.67
ATOM	234	C	THR	A	37	26.587	-2.513	12.350	1.00	15.44
ATOM	235	O	THR	A	37	27.040	-3.055	13.410	1.00	20.20
ATOM	236	CB	THR	A	37	26.592	-2.679	9.818	1.00	14.13
ATOM	237	OG1	THR	A	37	25.241	-2.212	9.503	1.00	22.62
ATOM	238	CG2	THR	A	37	26.949	-3.739	8.800	1.00	2.29
ATOM	239	N	VAL	A	38	25.733	-1.493	12.249	1.00	11.92

ATOM	240	CA	VAL	A	38	25.237	-0.800	13.411	1.00	15.22
ATOM	241	C	VAL	A	38	24.588	-1.455	14.612	1.00	14.68
ATOM	242	O	VAL	A	38	24.906	-1.185	15.733	1.00	15.89
ATOM	243	CB	VAL	A	38	24.124	0.180	12.855	1.00	14.13
ATOM	244	CG1	VAL	A	38	23.663	0.897	14.167	1.00	13.55
ATOM	245	CG2	VAL	A	38	24.570	1.025	11.670	1.00	6.75
ATOM	246	N	GLY	A	39	23.745	-2.410	14.677	1.00	14.24
ATOM	247	CA	GLY	A	39	23.135	-3.151	15.746	1.00	11.03
ATOM	248	C	GLY	A	39	24.096	-3.586	16.791	1.00	13.34
ATOM	249	O	GLY	A	39	24.131	-3.181	17.934	1.00	15.13
ATOM	250	N	PRO	A	40	25.067	-4.340	16.352	1.00	14.70
ATOM	251	CA	PRO	A	40	26.094	-5.025	17.171	1.00	13.44
ATOM	252	C	PRO	A	40	27.010	-3.909	17.589	1.00	11.81
ATOM	253	O	PRO	A	40	27.346	-3.871	18.764	1.00	12.79
ATOM	254	CB	PRO	A	40	26.723	-6.111	16.279	1.00	8.43
ATOM	255	CG	PRO	A	40	25.873	-6.243	14.950	1.00	4.84
ATOM	256	CD	PRO	A	40	25.198	-4.902	14.995	1.00	12.36
ATOM	257	N	ALA	A	41	27.226	-2.979	16.695	1.00	7.41
ATOM	258	CA	ALA	A	41	28.066	-1.962	17.278	1.00	11.03
ATOM	259	C	ALA	A	41	27.378	-1.206	18.439	1.00	14.87
ATOM	260	O	ALA	A	41	28.028	-0.503	19.274	1.00	14.26
ATOM	261	CB	ALA	A	41	28.579	-0.905	16.313	1.00	7.17
ATOM	262	N	LEU	A	42	26.135	-0.811	18.237	1.00	11.87
ATOM	263	CA	LEU	A	42	25.487	-0.048	19.300	1.00	12.36
ATOM	264	C	LEU	A	42	25.337	-0.856	20.624	1.00	11.94
ATOM	265	O	LEU	A	42	25.423	-0.397	21.730	1.00	8.33
ATOM	266	CB	LEU	A	42	24.036	0.168	18.811	1.00	13.24
ATOM	267	CG	LEU	A	42	23.272	1.160	19.676	1.00	6.90
ATOM	268	CD1	LEU	A	42	24.108	2.419	19.962	1.00	6.62
ATOM	269	CD2	LEU	A	42	21.991	1.580	18.943	1.00	7.11
ATOM	270	N	ALA	A	43	24.905	-2.095	20.482	1.00	10.88
ATOM	271	CA	ALA	A	43	24.761	-3.027	21.553	1.00	12.37
ATOM	272	C	ALA	A	43	26.106	-3.136	22.252	1.00	15.45
ATOM	273	O	ALA	A	43	25.958	-2.743	23.433	1.00	20.80
ATOM	274	CB	ALA	A	43	24.148	-4.324	21.002	1.00	9.60
ATOM	275	N	ASN	A	44	27.263	-3.440	21.636	1.00	16.91
ATOM	276	CA	ASN	A	44	28.454	-3.434	22.439	1.00	20.33
ATOM	277	C	ASN	A	44	28.717	-2.044	23.113	1.00	17.66
ATOM	278	O	ASN	A	44	29.019	-1.991	24.301	1.00	17.06
ATOM	279	CB	ASN	A	44	29.756	-3.695	21.625	1.00	35.48
ATOM	280	CG	ASN	A	44	29.564	-5.115	21.138	1.00	58.23
ATOM	281	OD1	ASN	A	44	30.013	-5.403	20.034	1.00	79.77
ATOM	282	ND2	ASN	A	44	28.908	-5.945	21.921	1.00	70.10
ATOM	283	N	GLY	A	45	28.682	-0.988	22.297	1.00	14.39
ATOM	284	CA	GLY	A	45	29.015	0.221	22.976	1.00	11.65
ATOM	285	C	GLY	A	45	28.175	0.255	24.234	1.00	14.30
ATOM	286	O	GLY	A	45	28.529	0.582	25.385	1.00	10.77
ATOM	287	N	LEU	A	46	26.861	0.099	24.065	1.00	16.88

ATOM	288	CA	LEU	A	46	25.968	0.248	25.207	1.00	16.29
ATOM	289	C	LEU	A	46	26.395	-0.651	26.346	1.00	13.48
ATOM	290	O	LEU	A	46	26.579	-0.325	27.462	1.00	7.75
ATOM	291	CB	LEU	A	46	24.608	-0.243	24.847	1.00	19.46
ATOM	292	CG	LEU	A	46	23.642	0.551	25.664	1.00	13.97
ATOM	293	CD1	LEU	A	46	24.089	1.994	25.563	1.00	13.99
ATOM	294	CD2	LEU	A	46	22.275	0.465	25.038	1.00	32.18
ATOM	295	N	GLU	A	47	26.523	-1.890	25.882	1.00	15.90
ATOM	296	CA	GLU	A	47	26.910	-2.886	26.909	1.00	24.03
ATOM	297	C	GLU	A	47	28.140	-2.500	27.702	1.00	24.14
ATOM	298	O	GLU	A	47	28.722	-3.203	28.500	1.00	27.24
ATOM	299	CB	GLU	A	47	27.147	-4.206	26.204	1.00	33.33
ATOM	300	CG	GLU	A	47	27.386	-5.254	27.245	1.00	51.29
ATOM	301	CD	GLU	A	47	27.661	-6.560	26.524	1.00	68.40
ATOM	302	OE1	GLU	A	47	26.741	-7.007	25.777	1.00	66.37
ATOM	303	OE2	GLU	A	47	28.856	-6.921	26.830	1.00	78.70
ATOM	304	N	SER	A	48	28.992	-1.626	27.215	1.00	27.50
ATOM	305	CA	SER	A	48	30.331	-1.518	27.789	1.00	25.23
ATOM	306	C	SER	A	48	30.108	-0.555	28.926	1.00	26.91
ATOM	307	O	SER	A	48	31.124	-0.058	29.462	1.00	33.39
ATOM	308	CB	SER	A	48	31.116	-0.990	26.621	1.00	21.90
ATOM	309	OG	SER	A	48	31.294	0.422	26.483	1.00	27.87
ATOM	310	N	HIS	A	49	28.826	-0.101	28.995	1.00	25.04
ATOM	311	CA	HIS	A	49	28.542	0.955	29.956	1.00	19.72
ATOM	312	C	HIS	A	49	27.480	0.461	30.950	1.00	22.55
ATOM	313	O	HIS	A	49	27.186	1.089	31.898	1.00	27.93
ATOM	314	CB	HIS	A	49	28.094	2.197	29.463	1.00	16.13
ATOM	315	CG	HIS	A	49	28.806	3.036	28.520	1.00	39.79
ATOM	316	ND1	HIS	A	49	29.564	4.058	28.953	1.00	45.66
ATOM	317	CD2	HIS	A	49	28.776	3.070	27.197	1.00	46.91
ATOM	318	CE1	HIS	A	49	30.028	4.750	27.979	1.00	45.87
ATOM	319	NE2	HIS	A	49	29.544	4.139	26.934	1.00	50.84
ATOM	320	N	ILE	A	50	27.009	-0.703	30.715	1.00	18.34
ATOM	321	CA	ILE	A	50	25.874	-1.129	31.415	1.00	19.89
ATOM	322	C	ILE	A	50	25.917	-2.629	31.146	1.00	26.29
ATOM	323	O	ILE	A	50	25.322	-3.023	30.168	1.00	25.33
ATOM	324	CB	ILE	A	50	24.527	-0.535	31.008	1.00	10.50
ATOM	325	CG1	ILE	A	50	24.340	0.906	31.292	1.00	4.97
ATOM	326	CG2	ILE	A	50	23.466	-1.298	31.697	1.00	12.96
ATOM	327	CD1	ILE	A	50	23.413	1.845	30.602	1.00	16.65
ATOM	328	N	ARG	A	51	26.707	-3.256	32.066	1.00	31.77
ATOM	329	CA	ARG	A	51	26.887	-4.714	32.107	1.00	29.06
ATOM	330	C	ARG	A	51	25.457	-5.331	32.170	1.00	32.68
ATOM	331	O	ARG	A	51	25.396	-6.363	31.512	1.00	37.16
ATOM	332	N	ASN	A	52	24.380	-4.817	32.788	1.00	28.48
ATOM	333	CA	ASN	A	52	23.284	-5.767	32.832	1.00	26.39
ATOM	334	C	ASN	A	52	22.176	-5.178	31.993	1.00	27.75
ATOM	335	O	ASN	A	52	21.333	-4.488	32.636	1.00	26.68

ATOM	336	CB	ASN	A	52	22.750	-5.884	34.232	1.00	34.86
ATOM	337	CG	ASN	A	52	21.637	-6.879	34.271	1.00	39.54
ATOM	338	OD1	ASN	A	52	20.781	-6.541	35.095	1.00	54.31
ATOM	339	ND2	ASN	A	52	21.611	-7.954	33.503	1.00	48.82
ATOM	340	N	ILE	A	53	22.127	-5.699	30.800	1.00	24.42
ATOM	341	CA	ILE	A	53	21.261	-5.092	29.772	1.00	20.15
ATOM	342	C	ILE	A	53	20.585	-6.151	28.912	1.00	17.63
ATOM	343	O	ILE	A	53	21.020	-7.349	28.917	1.00	18.01
ATOM	344	CB	ILE	A	53	22.245	-4.297	28.880	1.00	14.09
ATOM	345	CG1	ILE	A	53	21.682	-3.257	27.936	1.00	22.91
ATOM	346	CG2	ILE	A	53	22.907	-5.321	27.946	1.00	16.37
ATOM	347	CD1	ILE	A	53	22.877	-2.315	27.622	1.00	38.17
ATOM	348	N	TRP	A	54	19.447	-5.880	28.383	1.00	15.19
ATOM	349	CA	TRP	A	54	18.804	-6.889	27.567	1.00	17.96
ATOM	350	C	TRP	A	54	18.803	-6.230	26.151	1.00	19.82
ATOM	351	O	TRP	A	54	18.340	-5.059	25.985	1.00	18.37
ATOM	352	CB	TRP	A	54	17.364	-7.046	27.998	1.00	23.18
ATOM	353	CG	TRP	A	54	16.949	-7.932	29.100	1.00	24.57
ATOM	354	CD1	TRP	A	54	17.757	-8.727	29.895	1.00	24.46
ATOM	355	CD2	TRP	A	54	15.595	-8.164	29.603	1.00	30.21
ATOM	356	NE1	TRP	A	54	17.004	-9.372	30.858	1.00	25.87
ATOM	357	CE2	TRP	A	54	15.692	-9.039	30.700	1.00	24.92
ATOM	358	CE3	TRP	A	54	14.358	-7.633	29.243	1.00	36.26
ATOM	359	CZ2	TRP	A	54	14.611	-9.442	31.432	1.00	19.75
ATOM	360	CZ3	TRP	A	54	13.316	-8.042	30.009	1.00	32.94
ATOM	361	CH2	TRP	A	54	13.451	-8.916	31.068	1.00	23.02
ATOM	362	N	ILE	A	55	19.063	-7.152	25.204	1.00	15.21
ATOM	363	CA	ILE	A	55	19.178	-6.655	23.838	1.00	12.41
ATOM	364	C	ILE	A	55	18.091	-7.215	22.962	1.00	11.40
ATOM	365	O	ILE	A	55	17.955	-8.378	22.680	1.00	7.34
ATOM	366	CB	ILE	A	55	20.546	-6.962	23.201	1.00	16.44
ATOM	367	CG1	ILE	A	55	21.939	-6.409	23.702	1.00	8.75
ATOM	368	CG2	ILE	A	55	20.384	-6.460	21.750	1.00	21.77
ATOM	369	CD1	ILE	A	55	21.767	-5.582	24.863	1.00	16.23
ATOM	370	N	GLN	A	56	17.226	-6.412	22.390	1.00	9.67
ATOM	371	CA	GLN	A	56	16.161	-7.016	21.619	1.00	10.90
ATOM	372	C	GLN	A	56	16.432	-6.621	20.143	1.00	13.08
ATOM	373	O	GLN	A	56	16.402	-5.393	19.953	1.00	10.32
ATOM	374	CB	GLN	A	56	14.786	-6.542	22.014	1.00	11.49
ATOM	375	CG	GLN	A	56	13.653	-7.256	21.316	1.00	23.47
ATOM	376	CD	GLN	A	56	13.789	-8.741	21.351	1.00	24.88
ATOM	377	OE1	GLN	A	56	13.610	-9.379	20.324	1.00	9.56
ATOM	378	NE2	GLN	A	56	14.119	-9.221	22.544	1.00	17.94
ATOM	379	N	GLY	A	57	16.288	-7.645	19.216	1.00	6.84
ATOM	380	CA	GLY	A	57	16.174	-7.019	17.841	1.00	16.15
ATOM	381	C	GLY	A	57	14.740	-7.085	17.267	1.00	13.72
ATOM	382	O	GLY	A	57	14.124	-8.016	17.752	1.00	12.70
ATOM	383	N	VAL	A	58	14.068	-6.264	16.525	1.00	12.73

ATOM	384	CA	VAL	A	58	12.739	-6.308	16.070	1.00	11.16
ATOM	385	C	VAL	A	58	12.715	-7.246	14.893	1.00	14.85
ATOM	386	O	VAL	A	58	13.234	-6.891	13.849	1.00	18.64
ATOM	387	CB	VAL	A	58	12.262	-4.984	15.352	1.00	6.54
ATOM	388	CG1	VAL	A	58	10.894	-4.974	14.731	1.00	5.89
ATOM	389	CG2	VAL	A	58	12.650	-3.840	16.331	1.00	5.86
ATOM	390	N	GLY	A	59	12.209	-8.465	15.008	1.00	21.96
ATOM	391	CA	GLY	A	59	12.120	-9.385	13.874	1.00	17.81
ATOM	392	C	GLY	A	59	10.645	-9.561	13.550	1.00	23.35
ATOM	393	O	GLY	A	59	9.919	-8.579	13.249	1.00	27.99
ATOM	394	N	GLY	A	60	10.166	-10.805	13.623	1.00	18.75
ATOM	395	CA	GLY	A	60	8.841	-11.142	13.285	1.00	11.46
ATOM	396	C	GLY	A	60	8.550	-10.833	11.851	1.00	14.56
ATOM	397	O	GLY	A	60	9.160	-11.439	11.003	1.00	16.32
ATOM	398	N	PRO	A	61	7.505	-10.103	11.612	1.00	12.10
ATOM	399	CA	PRO	A	61	7.123	-9.774	10.250	1.00	14.70
ATOM	400	C	PRO	A	61	8.230	-8.941	9.570	1.00	22.17
ATOM	401	O	PRO	A	61	8.143	-8.758	8.344	1.00	25.74
ATOM	402	CB	PRO	A	61	5.911	-8.860	10.332	1.00	14.30
ATOM	403	CG	PRO	A	61	5.880	-8.514	11.784	1.00	13.62
ATOM	404	CD	PRO	A	61	6.723	-9.417	12.576	1.00	12.29
ATOM	405	N	TYR	A	62	9.162	-8.257	10.292	1.00	21.56
ATOM	406	CA	TYR	A	62	9.973	-7.242	9.674	1.00	17.07
ATOM	407	C	TYR	A	62	11.133	-7.907	9.047	1.00	18.73
ATOM	408	O	TYR	A	62	12.132	-8.213	9.691	1.00	22.39
ATOM	409	CB	TYR	A	62	10.504	-6.401	10.803	1.00	17.51
ATOM	410	CG	TYR	A	62	11.461	-5.421	10.236	1.00	15.23
ATOM	411	CD1	TYR	A	62	11.343	-4.920	9.032	1.00	17.79
ATOM	412	CD2	TYR	A	62	12.465	-4.971	10.969	1.00	19.09
ATOM	413	CE1	TYR	A	62	12.206	-3.997	8.506	1.00	19.28
ATOM	414	CE2	TYR	A	62	13.438	-4.101	10.490	1.00	25.40
ATOM	415	CZ	TYR	A	62	13.327	-3.571	9.186	1.00	20.95
ATOM	416	OH	TYR	A	62	14.320	-2.649	8.791	1.00	14.70
ATOM	417	N	ASP	A	63	10.998	-8.419	7.816	1.00	19.47
ATOM	418	CA	ASP	A	63	12.137	-9.011	7.081	1.00	17.52
ATOM	419	C	ASP	A	63	13.027	-7.973	6.453	1.00	17.97
ATOM	420	O	ASP	A	63	13.628	-8.442	5.512	1.00	14.94
ATOM	421	CB	ASP	A	63	11.474	-9.873	6.015	1.00	17.16
ATOM	422	CG	ASP	A	63	10.563	-9.136	5.096	1.00	27.75
ATOM	423	OD1	ASP	A	63	10.049	-8.030	5.281	1.00	34.11
ATOM	424	OD2	ASP	A	63	10.300	-9.635	4.002	1.00	44.13
ATOM	425	N	ALA	A	64	13.089	-6.685	6.584	1.00	15.36
ATOM	426	CA	ALA	A	64	14.054	-5.725	6.098	1.00	17.14
ATOM	427	C	ALA	A	64	14.118	-5.780	4.589	1.00	21.10
ATOM	428	O	ALA	A	64	15.193	-5.861	3.968	1.00	23.12
ATOM	429	CB	ALA	A	64	15.458	-5.861	6.646	1.00	20.45
ATOM	430	N	ALA	A	65	12.946	-6.009	4.006	1.00	22.21
ATOM	431	CA	ALA	A	65	12.817	-6.072	2.565	1.00	21.81

ATOM	432	C	ALA	A	65	13.143	-4.857	1.745	1.00	21.76
ATOM	433	O	ALA	A	65	12.855	-3.801	2.229	1.00	23.60
ATOM	434	CB	ALA	A	65	11.384	-6.390	2.364	1.00	17.31
ATOM	435	N	LEU	A	66	13.401	-4.866	0.402	1.00	21.48
ATOM	436	CA	LEU	A	66	13.763	-3.581	-0.216	1.00	13.20
ATOM	437	C	LEU	A	66	12.469	-2.913	-0.452	1.00	13.90
ATOM	438	O	LEU	A	66	12.548	-1.767	-0.197	1.00	11.85
ATOM	439	CB	LEU	A	66	14.593	-3.602	-1.470	1.00	3.92
ATOM	440	CG	LEU	A	66	15.891	-4.308	-1.191	1.00	9.05
ATOM	441	CD1	LEU	A	66	16.509	-4.725	-2.438	1.00	12.78
ATOM	442	CD2	LEU	A	66	16.569	-3.119	-0.580	1.00	13.44
ATOM	443	N	ALA	A	67	11.413	-3.625	-0.801	1.00	14.94
ATOM	444	CA	ALA	A	67	10.253	-2.759	-1.277	1.00	12.42
ATOM	445	C	ALA	A	67	9.626	-1.879	-0.224	1.00	14.21
ATOM	446	O	ALA	A	67	9.218	-0.818	-0.643	1.00	14.29
ATOM	447	CB	ALA	A	67	9.089	-3.588	-1.781	1.00	3.90
ATOM	448	N	THR	A	68	9.494	-2.409	1.006	1.00	12.11
ATOM	449	CA	THR	A	68	8.780	-1.647	1.997	1.00	11.77
ATOM	450	C	THR	A	68	9.242	-0.214	2.219	1.00	13.05
ATOM	451	O	THR	A	68	8.597	0.683	2.766	1.00	11.13
ATOM	452	CB	THR	A	68	8.892	-2.488	3.241	1.00	13.93
ATOM	453	OG1	THR	A	68	10.145	-3.150	3.224	1.00	27.44
ATOM	454	CG2	THR	A	68	7.783	-3.459	3.087	1.00	13.39
ATOM	455	N	ASN	A	69	10.450	-0.057	1.808	1.00	7.59
ATOM	456	CA	ASN	A	69	11.020	1.236	1.791	1.00	8.76
ATOM	457	C	ASN	A	69	10.095	2.165	1.047	1.00	10.28
ATOM	458	O	ASN	A	69	9.950	3.345	1.305	1.00	5.30
ATOM	459	CB	ASN	A	69	12.461	1.251	1.231	1.00	5.54
ATOM	460	CG	ASN	A	69	13.374	1.207	2.398	1.00	15.08
ATOM	461	OD1	ASN	A	69	13.307	2.124	3.275	1.00	31.90
ATOM	462	ND2	ASN	A	69	14.048	0.099	2.360	1.00	4.51
ATOM	463	N	PHE	A	70	9.390	1.656	0.079	1.00	19.09
ATOM	464	CA	PHE	A	70	8.552	2.619	-0.631	1.00	21.80
ATOM	465	C	PHE	A	70	7.157	2.836	-0.123	1.00	23.36
ATOM	466	O	PHE	A	70	6.509	3.717	-0.724	1.00	25.74
ATOM	467	CB	PHE	A	70	8.547	2.386	-2.082	1.00	17.38
ATOM	468	CG	PHE	A	70	9.870	2.360	-2.770	1.00	15.72
ATOM	469	CD1	PHE	A	70	10.080	3.430	-3.576	1.00	5.15
ATOM	470	CD2	PHE	A	70	10.702	1.245	-2.497	1.00	7.61
ATOM	471	CE1	PHE	A	70	11.268	3.330	-4.191	1.00	16.05
ATOM	472	CE2	PHE	A	70	11.913	1.267	-3.168	1.00	22.23
ATOM	473	CZ	PHE	A	70	12.199	2.314	-4.016	1.00	9.57
ATOM	474	N	LEU	A	71	6.765	2.246	1.034	1.00	25.53
ATOM	475	CA	LEU	A	71	5.506	2.725	1.599	1.00	24.24
ATOM	476	C	LEU	A	71	5.649	4.037	2.343	1.00	27.91
ATOM	477	O	LEU	A	71	6.694	4.521	2.750	1.00	28.86
ATOM	478	CB	LEU	A	71	5.150	1.635	2.535	1.00	19.99
ATOM	479	CG	LEU	A	71	5.003	0.342	1.873	1.00	16.09

ATOM	480	CD1	LEU	A	71	4.879	-0.764	2.885	1.00	18.12
ATOM	481	CD2	LEU	A	71	3.786	0.546	1.000	1.00	18.24
ATOM	482	N	PRO	A	72	4.535	4.663	2.529	1.00	33.01
ATOM	483	CA	PRO	A	72	4.389	5.888	3.311	1.00	34.96
ATOM	484	C	PRO	A	72	4.865	5.590	4.778	1.00	32.90
ATOM	485	O	PRO	A	72	4.619	4.512	5.331	1.00	28.55
ATOM	486	CB	PRO	A	72	2.983	6.453	3.095	1.00	32.98
ATOM	487	CG	PRO	A	72	2.224	5.189	2.827	1.00	30.36
ATOM	488	CD	PRO	A	72	3.188	4.093	2.380	1.00	33.56
ATOM	489	N	ARG	A	73	5.601	6.610	5.221	1.00	27.54
ATOM	490	CA	ARG	A	73	6.325	6.547	6.408	1.00	25.42
ATOM	491	C	ARG	A	73	7.613	5.755	6.321	1.00	21.78
ATOM	492	O	ARG	A	73	8.360	5.950	7.304	1.00	29.61
ATOM	493	CB	ARG	A	73	5.469	5.978	7.549	1.00	24.29
ATOM	494	CG	ARG	A	73	4.575	6.998	8.155	1.00	23.47
ATOM	495	CD	ARG	A	73	3.818	6.793	9.360	1.00	29.73
ATOM	496	NE	ARG	A	73	3.222	5.460	9.392	1.00	36.30
ATOM	497	CZ	ARG	A	73	2.891	5.312	10.713	1.00	42.26
ATOM	498	NH1	ARG	A	73	3.145	6.288	11.555	1.00	26.57
ATOM	499	NH2	ARG	A	73	2.320	4.144	10.883	1.00	39.03
ATOM	500	N	GLY	A	74	7.868	4.909	5.326	1.00	8.42
ATOM	501	CA	GLY	A	74	9.120	4.291	5.332	1.00	5.06
ATOM	502	C	GLY	A	74	9.243	2.858	5.508	1.00	12.74
ATOM	503	O	GLY	A	74	10.256	2.286	5.317	1.00	16.46
ATOM	504	N	THR	A	75	8.145	2.321	5.906	1.00	12.82
ATOM	505	CA	THR	A	75	8.036	0.869	6.008	1.00	11.14
ATOM	506	C	THR	A	75	6.625	0.428	6.134	1.00	10.64
ATOM	507	O	THR	A	75	5.757	1.231	5.949	1.00	9.36
ATOM	508	CB	THR	A	75	8.843	0.398	7.219	1.00	6.97
ATOM	509	OG1	THR	A	75	8.938	-0.950	7.125	1.00	5.64
ATOM	510	CG2	THR	A	75	8.108	0.865	8.603	1.00	6.30
ATOM	511	N	SER	A	76	6.409	-0.858	6.259	1.00	10.07
ATOM	512	CA	SER	A	76	5.061	-1.384	6.354	1.00	13.33
ATOM	513	C	SER	A	76	4.405	-1.163	7.747	1.00	21.87
ATOM	514	O	SER	A	76	5.228	-1.102	8.679	1.00	24.22
ATOM	515	CB	SER	A	76	5.030	-2.832	6.083	1.00	4.81
ATOM	516	OG	SER	A	76	5.327	-3.664	7.107	1.00	16.98
ATOM	517	N	GLN	A	77	3.082	-1.100	7.911	1.00	24.90
ATOM	518	CA	GLN	A	77	2.454	-1.020	9.166	1.00	23.85
ATOM	519	C	GLN	A	77	2.643	-2.236	10.015	1.00	19.58
ATOM	520	O	GLN	A	77	2.908	-2.140	11.203	1.00	15.15
ATOM	521	CB	GLN	A	77	0.983	-0.703	9.217	1.00	32.64
ATOM	522	CG	GLN	A	77	0.567	-0.580	10.642	1.00	49.56
ATOM	523	CD	GLN	A	77	0.689	0.785	11.194	1.00	65.91
ATOM	524	OE1	GLN	A	77	0.956	0.869	12.356	1.00	66.06
ATOM	525	NE2	GLN	A	77	0.481	1.750	10.350	1.00	68.91
ATOM	526	N	ALA	A	78	2.754	-3.376	9.402	1.00	15.90
ATOM	527	CA	ALA	A	78	3.071	-4.577	10.073	1.00	19.47

ATOM	528	C	ALA	A	78	4.381	-4.332	10.819	1.00	24.48
ATOM	529	O	ALA	A	78	4.389	-4.729	11.983	1.00	26.91
ATOM	530	CB	ALA	A	78	3.390	-5.808	9.336	1.00	17.23
ATOM	531	N	ASN	A	79	5.350	-3.863	10.093	1.00	21.58
ATOM	532	CA	ASN	A	79	6.602	-3.576	10.774	1.00	20.62
ATOM	533	C	ASN	A	79	6.480	-2.673	11.969	1.00	20.93
ATOM	534	O	ASN	A	79	6.975	-2.944	13.053	1.00	15.52
ATOM	535	CB	ASN	A	79	7.474	-3.069	9.670	1.00	24.79
ATOM	536	CG	ASN	A	79	7.933	-4.238	8.824	1.00	28.76
ATOM	537	OD1	ASN	A	79	7.867	-5.439	9.091	1.00	25.30
ATOM	538	ND2	ASN	A	79	8.488	-3.891	7.660	1.00	24.90
ATOM	539	N	ILE	A	80	5.731	-1.611	11.936	1.00	15.93
ATOM	540	CA	ILE	A	80	5.586	-0.574	12.924	1.00	17.00
ATOM	541	C	ILE	A	80	4.925	-1.187	14.118	1.00	20.63
ATOM	542	O	ILE	A	80	5.234	-0.939	15.264	1.00	18.79
ATOM	543	CB	ILE	A	80	4.756	0.629	12.436	1.00	11.98
ATOM	544	CG1	ILE	A	80	5.627	1.124	11.297	1.00	9.50
ATOM	545	CG2	ILE	A	80	4.379	1.728	13.354	1.00	16.27
ATOM	546	CD1	ILE	A	80	5.007	2.071	10.424	1.00	8.15
ATOM	547	N	ASP	A	81	4.017	-2.019	13.708	1.00	19.21
ATOM	548	CA	ASP	A	81	3.304	-2.778	14.728	1.00	15.15
ATOM	549	C	ASP	A	81	4.147	-3.711	15.510	1.00	15.77
ATOM	550	O	ASP	A	81	4.084	-3.697	16.695	1.00	15.82
ATOM	551	CB	ASP	A	81	2.291	-3.438	13.868	1.00	26.36
ATOM	552	CG	ASP	A	81	1.065	-2.530	13.790	1.00	23.71
ATOM	553	OD1	ASP	A	81	1.105	-1.355	14.226	1.00	14.33
ATOM	554	OD2	ASP	A	81	0.061	-3.125	13.222	1.00	33.05
ATOM	555	N	GLU	A	82	5.148	-4.447	15.096	1.00	16.07
ATOM	556	CA	GLU	A	82	5.984	-5.318	15.882	1.00	14.77
ATOM	557	C	GLU	A	82	6.839	-4.355	16.667	1.00	19.33
ATOM	558	O	GLU	A	82	7.315	-4.708	17.752	1.00	23.58
ATOM	559	CB	GLU	A	82	6.998	-6.031	15.064	1.00	13.20
ATOM	560	CG	GLU	A	82	7.792	-7.239	15.476	1.00	23.09
ATOM	561	CD	GLU	A	82	6.767	-8.114	16.185	1.00	29.68
ATOM	562	OE1	GLU	A	82	5.666	-7.670	16.403	1.00	26.63
ATOM	563	OE2	GLU	A	82	7.273	-9.181	16.411	1.00	33.08
ATOM	564	N	GLY	A	83	7.228	-3.227	16.199	1.00	16.79
ATOM	565	CA	GLY	A	83	8.033	-2.428	17.140	1.00	17.32
ATOM	566	C	GLY	A	83	7.238	-2.018	18.366	1.00	17.54
ATOM	567	O	GLY	A	83	7.561	-2.103	19.528	1.00	15.06
ATOM	568	N	LYS	A	84	6.093	-1.408	18.114	1.00	18.72
ATOM	569	CA	LYS	A	84	5.050	-1.146	19.096	1.00	16.90
ATOM	570	C	LYS	A	84	4.893	-2.337	20.057	1.00	17.74
ATOM	571	O	LYS	A	84	4.962	-2.265	21.295	1.00	14.31
ATOM	572	CB	LYS	A	84	3.799	-0.872	18.307	1.00	14.62
ATOM	573	CG	LYS	A	84	3.535	0.565	18.291	1.00	19.30
ATOM	574	CD	LYS	A	84	2.787	1.013	17.044	1.00	34.24
ATOM	575	CE	LYS	A	84	1.568	1.902	17.337	1.00	37.70

ATOM	576	NZ	LYS	A	84	0.346	1.226	16.827	1.00	48.42
ATOM	577	N	ARG	A	85	4.617	-3.506	19.519	1.00	18.50
ATOM	578	CA	ARG	A	85	4.583	-4.705	20.280	1.00	19.04
ATOM	579	C	ARG	A	85	5.677	-4.733	21.308	1.00	19.63
ATOM	580	O	ARG	A	85	5.442	-5.192	22.383	1.00	19.24
ATOM	581	CB	ARG	A	85	4.740	-5.979	19.464	1.00	14.74
ATOM	582	CG	ARG	A	85	3.843	-7.094	19.887	1.00	8.85
ATOM	583	CD	ARG	A	85	4.146	-8.554	19.705	1.00	7.20
ATOM	584	NE	ARG	A	85	5.483	-8.898	19.194	1.00	20.30
ATOM	585	CZ	ARG	A	85	6.170	-9.705	19.899	1.00	18.19
ATOM	586	NH1	ARG	A	85	5.627	-10.161	21.040	1.00	34.03
ATOM	587	NH2	ARG	A	85	7.345	-9.979	19.555	1.00	15.36
ATOM	588	N	LEU	A	86	6.901	-4.586	20.956	1.00	22.21
ATOM	589	CA	LEU	A	86	8.006	-4.792	21.873	1.00	20.94
ATOM	590	C	LEU	A	86	8.044	-3.637	22.803	1.00	20.73
ATOM	591	O	LEU	A	86	8.155	-3.970	23.925	1.00	22.18
ATOM	592	CB	LEU	A	86	9.333	-4.932	21.168	1.00	6.67
ATOM	593	CG	LEU	A	86	9.358	-6.241	20.282	1.00	11.45
ATOM	594	CD1	LEU	A	86	10.546	-6.054	19.287	1.00	18.60
ATOM	595	CD2	LEU	A	86	9.362	-7.516	21.020	1.00	5.17
ATOM	596	N	PHE	A	87	7.700	-2.446	22.529	1.00	16.79
ATOM	597	CA	PHE	A	87	7.850	-1.416	23.492	1.00	18.21
ATOM	598	C	PHE	A	87	6.939	-1.805	24.618	1.00	26.51
ATOM	599	O	PHE	A	87	7.082	-1.565	25.839	1.00	30.36
ATOM	600	CB	PHE	A	87	7.498	-0.118	22.846	1.00	15.81
ATOM	601	CG	PHE	A	87	8.661	0.503	22.128	1.00	22.72
ATOM	602	CD1	PHE	A	87	9.625	1.163	22.795	1.00	25.90
ATOM	603	CD2	PHE	A	87	8.800	0.446	20.774	1.00	24.19
ATOM	604	CE1	PHE	A	87	10.699	1.781	22.220	1.00	26.46
ATOM	605	CE2	PHE	A	87	9.871	0.991	20.153	1.00	29.24
ATOM	606	CZ	PHE	A	87	10.827	1.669	20.849	1.00	20.81
ATOM	607	N	ALA	A	88	5.862	-2.422	24.266	1.00	29.15
ATOM	608	CA	ALA	A	88	4.772	-2.699	25.195	1.00	22.92
ATOM	609	C	ALA	A	88	5.186	-3.837	26.068	1.00	22.03
ATOM	610	O	ALA	A	88	4.974	-3.879	27.284	1.00	27.02
ATOM	611	CB	ALA	A	88	3.551	-2.803	24.299	1.00	22.13
ATOM	612	N	LEU	A	89	5.649	-4.897	25.531	1.00	19.16
ATOM	613	CA	LEU	A	89	6.188	-6.032	26.208	1.00	19.29
ATOM	614	C	LEU	A	89	7.250	-5.507	27.133	1.00	22.06
ATOM	615	O	LEU	A	89	7.449	-6.050	28.177	1.00	20.49
ATOM	616	CB	LEU	A	89	7.021	-6.863	25.221	1.00	18.41
ATOM	617	CG	LEU	A	89	7.477	-8.167	25.834	1.00	20.45
ATOM	618	CD1	LEU	A	89	6.326	-8.707	26.627	1.00	17.22
ATOM	619	CD2	LEU	A	89	8.060	-9.057	24.769	1.00	18.83
ATOM	620	N	ALA	A	90	8.124	-4.644	26.722	1.00	22.80
ATOM	621	CA	ALA	A	90	9.027	-4.137	27.701	1.00	24.14
ATOM	622	C	ALA	A	90	8.237	-3.488	28.849	1.00	23.63
ATOM	623	O	ALA	A	90	8.414	-3.835	30.071	1.00	22.73

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ATOM    624  CB  ALA A  90      10.080  -3.253  27.139  1.00  7.74
ATOM    625  N   ASN A  91       7.457  -2.445  28.732  1.00 25.45
ATOM    626  CA  ASN A  91       6.665  -1.979  29.870  1.00 27.25
ATOM    627  C   ASN A  91       5.847  -2.996  30.656  1.00 30.97
ATOM    628  O   ASN A  91       5.346  -2.884  31.768  1.00 27.64
ATOM    629  CB  ASN A  91       5.560  -1.206  29.125  1.00 29.14
ATOM    630  CG  ASN A  91       4.946  -0.345  30.216  1.00 31.73
ATOM    631  OD1 ASN A  91       3.845  -0.692  30.645  1.00 46.76
ATOM    632  ND2 ASN A  91       5.641   0.629  30.643  1.00 29.03
ATOM    633  N   GLN A  92       5.369  -4.008  29.969  1.00 35.37
ATOM    634  CA  GLN A  92       4.702  -5.141  30.591  1.00 35.55
ATOM    635  C   GLN A  92       5.619  -6.072  31.352  1.00 34.28
ATOM    636  O   GLN A  92       5.227  -6.519  32.440  1.00 39.47
ATOM    637  CB  GLN A  92       3.866  -5.903  29.573  1.00 54.94
ATOM    638  CG  GLN A  92       2.689  -6.698  30.142  1.00 78.63
ATOM    639  CD  GLN A  92       2.806  -8.167  29.805  1.00 93.87
ATOM    640  OE1 GLN A  92       3.597  -8.840  30.475  1.00 96.99
ATOM    641  NE2 GLN A  92       2.083  -8.696  28.824  1.00 97.81
ATOM    642  N   LYS A  93       6.859  -6.403  31.050  1.00 31.97
ATOM    643  CA  LYS A  93       7.675  -7.204  31.972  1.00 25.22
ATOM    644  C   LYS A  93       8.381  -6.298  33.015  1.00 24.68
ATOM    645  O   LYS A  93       8.716  -6.793  34.075  1.00 32.13
ATOM    646  CB  LYS A  93       8.673  -7.980  31.148  1.00 10.86
ATOM    647  CG  LYS A  93       8.225  -8.963  30.159  1.00 24.26
ATOM    648  CD  LYS A  93       9.362  -9.966  29.986  1.00 21.96
ATOM    649  CE  LYS A  93       9.093 -10.718  28.658  1.00 23.78
ATOM    650  NZ  LYS A  93      10.084 -11.805  28.300  1.00 25.87
ATOM    651  N   CYS A  94       8.752  -5.096  32.774  1.00 16.62
ATOM    652  CA  CYS A  94       9.752  -4.412  33.480  1.00 18.95
ATOM    653  C   CYS A  94       9.512  -2.936  33.537  1.00 24.83
ATOM    654  O   CYS A  94      10.184  -2.017  33.150  1.00 26.80
ATOM    655  CB  CYS A  94      11.147  -4.691  32.911  1.00  3.14
ATOM    656  SG  CYS A  94      11.618  -6.437  32.882  1.00 25.28
ATOM    657  N   PRO A  95       8.403  -2.561  34.086  1.00 26.08
ATOM    658  CA  PRO A  95       7.891  -1.202  33.878  1.00 26.11
ATOM    659  C   PRO A  95       8.960  -0.259  34.299  1.00 27.32
ATOM    660  O   PRO A  95       8.776   0.966  34.108  1.00 29.08
ATOM    661  CB  PRO A  95       6.609  -1.090  34.747  1.00 20.75
ATOM    662  CG  PRO A  95       6.587  -2.421  35.322  1.00 19.04
ATOM    663  CD  PRO A  95       7.363  -3.461  34.509  1.00 22.55
ATOM    664  N   ASN A  96       9.836  -0.776  35.193  1.00 31.44
ATOM    665  CA  ASN A  96      10.559   0.274  35.966  1.00 35.38
ATOM    666  C   ASN A  96      11.891   0.476  35.353  1.00 33.83
ATOM    667  O   ASN A  96      12.599   1.359  35.684  1.00 33.31
ATOM    668  CB  ASN A  96      10.558  -0.099  37.429  1.00 53.70
ATOM    669  CG  ASN A  96       9.238   0.342  38.026  1.00 61.69
ATOM    670  OD1 ASN A  96       8.758   1.432  37.706  1.00 64.33
ATOM    671  ND2 ASN A  96       8.676  -0.526  38.861  1.00 67.25
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ATOM	672	N	THR	A	97	12.287	-0.409	34.507	1.00	30.32
ATOM	673	CA	THR	A	97	13.519	-0.367	33.794	1.00	22.83
ATOM	674	C	THR	A	97	13.404	0.493	32.534	1.00	22.44
ATOM	675	O	THR	A	97	12.446	0.779	31.816	1.00	21.14
ATOM	676	CB	THR	A	97	13.835	-1.851	33.705	1.00	25.87
ATOM	677	OG1	THR	A	97	14.602	-1.915	32.528	1.00	38.91
ATOM	678	CG2	THR	A	97	12.769	-2.901	33.621	1.00	24.22
ATOM	679	N	PRO	A	98	14.393	1.415	32.408	1.00	20.59
ATOM	680	CA	PRO	A	98	14.513	2.292	31.254	1.00	18.15
ATOM	681	C	PRO	A	98	14.882	1.494	29.978	1.00	16.07
ATOM	682	O	PRO	A	98	15.622	0.462	29.934	1.00	17.19
ATOM	683	CB	PRO	A	98	15.563	3.339	31.676	1.00	14.55
ATOM	684	CG	PRO	A	98	16.270	2.646	32.699	1.00	12.29
ATOM	685	CD	PRO	A	98	15.735	1.331	33.046	1.00	12.02
ATOM	686	N	VAL	A	99	14.322	2.107	28.940	1.00	13.81
ATOM	687	CA	VAL	A	99	14.225	1.544	27.632	1.00	14.02
ATOM	688	C	VAL	A	99	14.956	2.407	26.663	1.00	10.66
ATOM	689	O	VAL	A	99	14.716	3.679	26.712	1.00	6.90
ATOM	690	CB	VAL	A	99	12.673	1.343	27.335	1.00	2.87
ATOM	691	CG1	VAL	A	99	12.666	1.272	25.872	1.00	17.40
ATOM	692	CG2	VAL	A	99	12.442	-0.111	27.744	1.00	5.75
ATOM	693	N	VAL	A	100	15.885	1.776	25.861	1.00	6.45
ATOM	694	CA	VAL	A	100	16.525	2.755	24.900	1.00	9.61
ATOM	695	C	VAL	A	100	16.389	2.159	23.561	1.00	10.79
ATOM	696	O	VAL	A	100	16.256	0.973	23.477	1.00	9.11
ATOM	697	CB	VAL	A	100	17.877	3.260	25.197	1.00	8.05
ATOM	698	CG1	VAL	A	100	17.824	4.252	26.336	1.00	6.05
ATOM	699	CG2	VAL	A	100	18.853	2.053	25.591	1.00	6.68
ATOM	700	N	ALA	A	101	16.277	2.928	22.511	1.00	13.14
ATOM	701	CA	ALA	A	101	16.127	2.266	21.183	1.00	15.67
ATOM	702	C	ALA	A	101	17.065	2.747	20.053	1.00	12.08
ATOM	703	O	ALA	A	101	17.261	4.042	19.907	1.00	11.16
ATOM	704	CB	ALA	A	101	14.685	2.609	20.812	1.00	6.57
ATOM	705	N	GLY	A	102	17.218	1.787	19.099	1.00	7.53
ATOM	706	CA	GLY	A	102	17.949	2.415	17.939	1.00	7.10
ATOM	707	C	GLY	A	102	17.477	1.803	16.744	1.00	7.27
ATOM	708	O	GLY	A	102	17.102	0.621	16.878	1.00	10.83
ATOM	709	N	GLY	A	103	17.706	2.407	15.648	1.00	7.80
ATOM	710	CA	GLY	A	103	17.446	1.745	14.356	1.00	5.33
ATOM	711	C	GLY	A	103	18.303	2.211	13.180	1.00	7.56
ATOM	712	O	GLY	A	103	18.785	3.340	13.227	1.00	6.88
ATOM	713	N	TYR	A	104	18.490	1.387	12.139	1.00	7.09
ATOM	714	CA	TYR	A	104	19.392	1.682	11.069	1.00	5.99
ATOM	715	C	TYR	A	104	18.705	1.614	9.705	1.00	9.47
ATOM	716	O	TYR	A	104	18.115	0.638	9.441	1.00	6.46
ATOM	717	CB	TYR	A	104	20.592	0.797	11.079	1.00	5.40
ATOM	718	CG	TYR	A	104	21.436	1.078	9.876	1.00	8.05
ATOM	719	CD1	TYR	A	104	21.708	2.302	9.352	1.00	5.91

ATOM	720	CD2	TYR	A	104	21.961	-0.044	9.172	1.00	6.85
ATOM	721	CE1	TYR	A	104	22.447	2.513	8.186	1.00	5.61
ATOM	722	CE2	TYR	A	104	22.751	0.052	8.072	1.00	7.49
ATOM	723	CZ	TYR	A	104	22.972	1.377	7.608	1.00	11.08
ATOM	724	OH	TYR	A	104	23.795	1.509	6.479	1.00	14.32
ATOM	725	N	SER	A	105	18.939	2.975	8.852	1.00	18.39
ATOM	726	CA	SER	A	105	18.190	2.854	7.601	1.00	9.66
ATOM	727	C	SER	A	105	16.763	2.370	7.722	1.00	6.10
ATOM	728	O	SER	A	105	16.090	3.304	8.077	1.00	5.63
ATOM	729	CB	SER	A	105	19.124	2.159	6.607	1.00	8.55
ATOM	730	OG	SER	A	105	18.553	1.685	5.463	1.00	24.30
ATOM	731	N	GLN	A	106	16.241	1.405	7.079	1.00	9.93
ATOM	732	CA	GLN	A	106	14.759	1.316	7.002	1.00	8.25
ATOM	733	C	GLN	A	106	14.453	1.089	8.473	1.00	8.51
ATOM	734	O	GLN	A	106	13.470	1.683	8.862	1.00	6.31
ATOM	735	CB	GLN	A	106	14.239	0.393	5.940	1.00	7.45
ATOM	736	CG	GLN	A	106	13.184	-0.528	6.465	1.00	18.04
ATOM	737	CD	GLN	A	106	12.228	-1.220	5.581	1.00	16.87
ATOM	738	OE1	GLN	A	106	11.024	-1.180	5.492	1.00	17.59
ATOM	739	NE2	GLN	A	106	12.643	-2.032	4.713	1.00	8.32
ATOM	740	N	GLY	A	107	15.269	0.310	9.172	1.00	7.13
ATOM	741	CA	GLY	A	107	15.190	0.159	10.606	1.00	4.61
ATOM	742	C	GLY	A	107	15.048	1.472	11.356	1.00	8.27
ATOM	743	O	GLY	A	107	14.219	1.511	12.290	1.00	6.52
ATOM	744	N	ALA	A	108	15.653	2.637	11.033	1.00	6.44
ATOM	745	CA	ALA	A	108	15.266	3.864	11.641	1.00	7.41
ATOM	746	C	ALA	A	108	13.813	4.346	11.471	1.00	11.76
ATOM	747	O	ALA	A	108	13.150	4.914	12.298	1.00	12.64
ATOM	748	CB	ALA	A	108	16.121	5.006	11.170	1.00	13.93
ATOM	749	N	ALA	A	109	13.321	4.312	10.267	1.00	9.78
ATOM	750	CA	ALA	A	109	12.056	4.685	9.861	1.00	10.47
ATOM	751	C	ALA	A	109	11.093	3.858	10.727	1.00	12.32
ATOM	752	O	ALA	A	109	10.016	4.391	11.035	1.00	14.67
ATOM	753	CB	ALA	A	109	12.035	4.173	8.456	1.00	10.24
ATOM	754	N	LEU	A	110	11.259	2.690	11.077	1.00	4.34
ATOM	755	CA	LEU	A	110	10.458	1.760	11.783	1.00	11.71
ATOM	756	C	LEU	A	110	10.305	2.253	13.203	1.00	15.26
ATOM	757	O	LEU	A	110	9.298	2.672	13.685	1.00	18.07
ATOM	758	CB	LEU	A	110	11.031	0.319	11.634	1.00	7.52
ATOM	759	CG	LEU	A	110	10.247	-0.801	12.258	1.00	8.41
ATOM	760	CD1	LEU	A	110	10.685	-2.233	11.862	1.00	7.17
ATOM	761	CD2	LEU	A	110	10.278	-0.659	13.783	1.00	5.25
ATOM	762	N	ILE	A	111	11.397	2.373	13.907	1.00	15.77
ATOM	763	CA	ILE	A	111	11.510	2.860	15.246	1.00	12.22
ATOM	764	C	ILE	A	111	11.027	4.255	15.234	1.00	9.39
ATOM	765	O	ILE	A	111	10.404	4.636	16.241	1.00	12.54
ATOM	766	CB	ILE	A	111	12.977	2.814	15.685	1.00	15.55
ATOM	767	CG1	ILE	A	111	13.222	1.279	15.805	1.00	14.19

ATOM	768	CG2	ILE	A	111	13.195	3.465	17.005	1.00	4.64
ATOM	769	CD1	ILE	A	111	12.410	0.887	17.002	1.00	14.88
ATOM	770	N	ALA	A	112	11.309	5.170	14.341	1.00	11.00
ATOM	771	CA	ALA	A	112	10.792	6.528	14.427	1.00	12.45
ATOM	772	C	ALA	A	112	9.266	6.455	14.308	1.00	15.59
ATOM	773	O	ALA	A	112	8.728	7.131	15.154	1.00	18.13
ATOM	774	CB	ALA	A	112	11.334	7.505	13.486	1.00	5.70
ATOM	775	N	ALA	A	113	8.575	5.572	13.587	1.00	12.85
ATOM	776	CA	ALA	A	113	7.167	5.512	13.557	1.00	15.39
ATOM	777	C	ALA	A	113	6.475	5.093	14.861	1.00	18.21
ATOM	778	O	ALA	A	113	5.498	5.750	15.226	1.00	14.59
ATOM	779	CB	ALA	A	113	6.678	4.562	12.500	1.00	17.63
ATOM	780	N	ALA	A	114	6.937	3.948	15.303	1.00	16.02
ATOM	781	CA	ALA	A	114	6.483	3.218	16.412	1.00	16.43
ATOM	782	C	ALA	A	114	6.578	4.114	17.643	1.00	22.20
ATOM	783	O	ALA	A	114	5.673	4.321	18.426	1.00	18.94
ATOM	784	CB	ALA	A	114	7.474	2.084	16.565	1.00	4.69
ATOM	785	N	VAL	A	115	7.722	4.836	17.744	1.00	22.46
ATOM	786	CA	VAL	A	115	7.855	5.499	19.064	1.00	20.88
ATOM	787	C	VAL	A	115	6.670	6.469	19.007	1.00	22.71
ATOM	788	O	VAL	A	115	6.136	6.761	20.057	1.00	22.05
ATOM	789	CB	VAL	A	115	9.279	6.090	19.137	1.00	19.61
ATOM	790	CG1	VAL	A	115	9.396	7.259	20.122	1.00	8.35
ATOM	791	CG2	VAL	A	115	10.245	5.016	19.562	1.00	13.91
ATOM	792	N	SER	A	116	6.467	7.085	17.828	1.00	23.59
ATOM	793	CA	SER	A	116	5.539	8.172	17.736	1.00	23.68
ATOM	794	C	SER	A	116	4.169	7.647	18.120	1.00	23.77
ATOM	795	O	SER	A	116	3.333	8.523	18.399	1.00	27.35
ATOM	796	CB	SER	A	116	5.522	8.865	16.376	1.00	25.21
ATOM	797	OG	SER	A	116	5.168	8.043	15.277	1.00	28.05
ATOM	798	N	GLU	A	117	3.859	6.397	18.004	1.00	18.83
ATOM	799	CA	GLU	A	117	2.491	6.020	18.238	1.00	22.21
ATOM	800	C	GLU	A	117	2.461	5.474	19.653	1.00	30.46
ATOM	801	O	GLU	A	117	1.487	4.773	19.863	1.00	35.72
ATOM	802	CB	GLU	A	117	1.977	4.902	17.343	1.00	21.63
ATOM	803	CG	GLU	A	117	2.167	5.219	15.897	1.00	26.41
ATOM	804	CD	GLU	A	117	1.560	4.424	14.814	1.00	34.01
ATOM	805	OE1	GLU	A	117	0.912	3.440	15.046	1.00	32.59
ATOM	806	OE2	GLU	A	117	1.750	4.833	13.659	1.00	44.62
ATOM	807	N	LEU	A	118	3.438	5.570	20.512	1.00	34.45
ATOM	808	CA	LEU	A	118	3.326	5.006	21.812	1.00	33.64
ATOM	809	C	LEU	A	118	2.681	6.110	22.633	1.00	41.75
ATOM	810	O	LEU	A	118	2.594	7.267	22.370	1.00	39.90
ATOM	811	CB	LEU	A	118	4.600	4.668	22.392	1.00	29.44
ATOM	812	CG	LEU	A	118	5.628	3.891	21.645	1.00	26.36
ATOM	813	CD1	LEU	A	118	6.921	3.840	22.379	1.00	27.53
ATOM	814	CD2	LEU	A	118	5.110	2.520	21.536	1.00	20.69
ATOM	815	N	SER	A	119	2.076	5.794	23.726	1.00	48.86

ATOM	816	CA	SER	A	119	0.910	5.647	24.476	1.00	52.44
ATOM	817	C	SER	A	119	1.212	6.063	25.866	1.00	52.57
ATOM	818	O	SER	A	119	1.485	5.258	26.735	1.00	55.54
ATOM	819	CB	SER	A	119	0.550	4.132	24.488	1.00	70.55
ATOM	820	OG	SER	A	119	1.393	3.091	23.908	1.00	66.80
ATOM	821	N	GLY	A	120	1.532	7.307	26.024	1.00	52.95
ATOM	822	CA	GLY	A	120	1.910	7.761	27.382	1.00	53.35
ATOM	823	C	GLY	A	120	2.944	7.109	28.291	1.00	49.09
ATOM	824	O	GLY	A	120	4.086	7.617	28.358	1.00	49.66
ATOM	825	N	ALA	A	121	2.526	6.129	29.102	1.00	42.97
ATOM	826	CA	ALA	A	121	3.477	5.574	30.022	1.00	40.72
ATOM	827	C	ALA	A	121	4.587	4.772	29.326	1.00	44.20
ATOM	828	O	ALA	A	121	5.749	4.803	29.711	1.00	45.42
ATOM	829	CB	ALA	A	121	2.965	4.542	30.903	1.00	36.34
ATOM	830	N	VAL	A	122	4.122	4.035	28.312	1.00	41.15
ATOM	831	CA	VAL	A	122	5.090	3.269	27.548	1.00	33.41
ATOM	832	C	VAL	A	122	5.870	4.168	26.652	1.00	28.48
ATOM	833	O	VAL	A	122	7.084	4.019	26.872	1.00	27.69
ATOM	834	CB	VAL	A	122	4.424	2.056	26.952	1.00	30.22
ATOM	835	CG1	VAL	A	122	2.924	1.997	27.098	1.00	28.03
ATOM	836	CG2	VAL	A	122	4.891	1.836	25.551	1.00	23.22
ATOM	837	N	LYS	A	123	5.424	5.310	26.177	1.00	23.16
ATOM	838	CA	LYS	A	123	6.354	6.314	25.661	1.00	23.11
ATOM	839	C	LYS	A	123	7.403	6.783	26.661	1.00	25.28
ATOM	840	O	LYS	A	123	8.524	7.224	26.449	1.00	29.01
ATOM	841	CB	LYS	A	123	5.561	7.502	25.100	1.00	23.54
ATOM	842	CG	LYS	A	123	6.171	8.573	24.277	1.00	26.71
ATOM	843	CD	LYS	A	123	5.400	9.775	23.888	1.00	43.07
ATOM	844	CE	LYS	A	123	4.953	9.783	22.461	1.00	59.59
ATOM	845	NZ	LYS	A	123	3.518	9.637	22.099	1.00	67.50
ATOM	846	N	GLU	A	124	6.977	6.991	27.918	1.00	27.95
ATOM	847	CA	GLU	A	124	7.845	7.700	28.863	1.00	27.29
ATOM	848	C	GLU	A	124	8.910	6.706	29.243	1.00	25.21
ATOM	849	O	GLU	A	124	9.993	7.165	29.769	1.00	21.21
ATOM	850	CB	GLU	A	124	6.986	8.351	29.927	1.00	40.13
ATOM	851	CG	GLU	A	124	7.588	8.609	31.295	1.00	57.40
ATOM	852	CD	GLU	A	124	8.530	9.814	31.247	1.00	66.99
ATOM	853	OE1	GLU	A	124	9.619	9.751	31.902	1.00	70.44
ATOM	854	OE2	GLU	A	124	7.949	10.652	30.502	1.00	73.84
ATOM	855	N	GLN	A	125	8.656	5.393	29.058	1.00	19.93
ATOM	856	CA	GLN	A	125	9.761	4.509	29.546	1.00	17.98
ATOM	857	C	GLN	A	125	10.865	4.556	28.521	1.00	24.28
ATOM	858	O	GLN	A	125	11.964	4.107	28.815	1.00	21.47
ATOM	859	CB	GLN	A	125	9.225	3.178	29.844	1.00	9.13
ATOM	860	CG	GLN	A	125	9.901	2.001	30.299	1.00	9.05
ATOM	861	CD	GLN	A	125	9.211	0.719	30.129	1.00	19.33
ATOM	862	OE1	GLN	A	125	8.190	0.703	29.466	1.00	28.52
ATOM	863	NE2	GLN	A	125	9.662	-0.396	30.684	1.00	13.34

ATOM	864	N	VAL	A	126	10.593	5.188	27.319	1.00 25.30
ATOM	865	CA	VAL	A	126	11.738	5.124	26.361	1.00 22.55
ATOM	866	C	VAL	A	126	12.546	6.334	26.614	1.00 17.55
ATOM	867	O	VAL	A	126	12.109	7.408	26.329	1.00 12.79
ATOM	868	CB	VAL	A	126	11.227	4.560	25.022	1.00 23.76
ATOM	869	CG1	VAL	A	126	9.706	4.686	24.946	1.00 23.77
ATOM	870	CG2	VAL	A	126	11.795	5.081	23.743	1.00 23.81
ATOM	871	N	LYS	A	127	13.726	6.233	27.264	1.00 16.41
ATOM	872	CA	LYS	A	127	14.462	7.494	27.639	1.00 18.18
ATOM	873	C	LYS	A	127	15.239	8.063	26.488	1.00 18.49
ATOM	874	O	LYS	A	127	15.812	9.103	26.680	1.00 18.99
ATOM	875	CB	LYS	A	127	15.401	7.148	28.792	1.00 20.81
ATOM	876	CG	LYS	A	127	14.770	6.110	29.713	1.00 21.99
ATOM	877	CD	LYS	A	127	13.435	6.726	30.064	1.00 33.86
ATOM	878	CE	LYS	A	127	12.779	6.612	31.399	1.00 32.17
ATOM	879	NZ	LYS	A	127	12.279	7.863	31.993	1.00 45.34
ATOM	880	N	GLY	A	128	15.522	7.281	25.416	1.00 20.56
ATOM	881	CA	GLY	A	128	16.280	7.948	24.306	1.00 20.72
ATOM	882	C	GLY	A	128	16.358	7.104	23.063	1.00 17.71
ATOM	883	O	GLY	A	128	16.168	5.901	23.226	1.00 16.66
ATOM	884	N	VAL	A	129	16.451	7.725	21.892	1.00 16.16
ATOM	885	CA	VAL	A	129	16.497	6.872	20.691	1.00 13.82
ATOM	886	C	VAL	A	129	17.519	7.371	19.719	1.00 8.35
ATOM	887	O	VAL	A	129	17.602	8.553	19.556	1.00 3.85
ATOM	888	CB	VAL	A	129	15.192	6.426	20.054	1.00 11.02
ATOM	889	CG1	VAL	A	129	14.007	7.041	20.726	1.00 6.50
ATOM	890	CG2	VAL	A	129	15.051	6.729	18.571	1.00 10.03
ATOM	891	N	ALA	A	130	18.455	6.398	19.363	1.00 8.05
ATOM	892	CA	ALA	A	130	19.430	6.845	18.344	1.00 7.55
ATOM	893	C	ALA	A	130	19.078	6.293	16.958	1.00 11.17
ATOM	894	O	ALA	A	130	18.755	5.145	16.849	1.00 15.74
ATOM	895	CB	ALA	A	130	20.781	6.391	18.603	1.00 5.89
ATOM	896	N	LEU	A	131	18.911	6.953	15.892	1.00 7.36
ATOM	897	CA	LEU	A	131	18.635	6.625	14.553	1.00 7.70
ATOM	898	C	LEU	A	131	19.876	6.908	13.661	1.00 12.02
ATOM	899	O	LEU	A	131	20.436	8.033	13.604	1.00 6.80
ATOM	900	CB	LEU	A	131	17.604	7.713	14.102	1.00 8.40
ATOM	901	CG	LEU	A	131	16.160	7.830	14.575	1.00 6.67
ATOM	902	CD1	LEU	A	131	15.391	8.957	13.981	1.00 4.49
ATOM	903	CD2	LEU	A	131	15.481	6.488	14.324	1.00 5.12
ATOM	904	N	PHE	A	132	20.271	6.009	12.802	1.00 11.56
ATOM	905	CA	PHE	A	132	21.422	6.183	11.908	1.00 10.44
ATOM	906	C	PHE	A	132	20.965	6.013	10.478	1.00 8.46
ATOM	907	O	PHE	A	132	20.175	5.101	10.097	1.00 11.04
ATOM	908	CB	PHE	A	132	22.217	4.931	12.282	1.00 10.56
ATOM	909	CG	PHE	A	132	22.693	4.830	13.714	1.00 16.38
ATOM	910	CD1	PHE	A	132	21.951	4.029	14.542	1.00 13.36
ATOM	911	CD2	PHE	A	132	23.860	5.489	14.213	1.00 15.12

ATOM	912	CE1	PHE	A	132	22.342	3.911	15.889	1.00	14.91
ATOM	913	CE2	PHE	A	132	24.176	5.323	15.513	1.00	18.02
ATOM	914	CZ	PHE	A	132	23.426	4.530	16.403	1.00	15.09
ATOM	915	N	GLY	A	133	21.431	6.876	9.580	1.00	7.35
ATOM	916	CA	GLY	A	133	21.026	6.893	8.148	1.00	5.86
ATOM	917	C	GLY	A	133	19.503	6.919	8.061	1.00	12.25
ATOM	918	O	GLY	A	133	18.890	5.926	7.593	1.00	9.03
ATOM	919	N	TYR	A	134	18.926	8.070	8.532	1.00	9.85
ATOM	920	CA	TYR	A	134	17.455	8.022	8.838	1.00	7.40
ATOM	921	C	TYR	A	134	16.647	8.365	7.584	1.00	10.61
ATOM	922	O	TYR	A	134	16.785	9.513	7.131	1.00	5.85
ATOM	923	CB	TYR	A	134	17.161	9.128	9.836	1.00	7.27
ATOM	924	CG	TYR	A	134	15.842	9.393	10.391	1.00	7.89
ATOM	925	CD1	TYR	A	134	14.889	8.437	10.312	1.00	6.65
ATOM	926	CD2	TYR	A	134	15.661	10.651	10.948	1.00	11.44
ATOM	927	CE1	TYR	A	134	13.657	8.690	10.821	1.00	9.05
ATOM	928	CE2	TYR	A	134	14.408	10.928	11.467	1.00	12.89
ATOM	929	CZ	TYR	A	134	13.428	9.923	11.423	1.00	14.22
ATOM	930	OH	TYR	A	134	12.146	10.110	11.975	1.00	12.41
ATOM	931	N	THR	A	135	15.811	7.398	7.139	1.00	11.51
ATOM	932	CA	THR	A	135	15.229	7.581	5.789	1.00	7.71
ATOM	933	C	THR	A	135	14.082	8.530	5.825	1.00	10.36
ATOM	934	O	THR	A	135	13.845	8.878	4.727	1.00	11.26
ATOM	935	CB	THR	A	135	14.772	6.394	4.967	1.00	12.02
ATOM	936	OG1	THR	A	135	13.821	5.399	5.398	1.00	22.81
ATOM	937	CG2	THR	A	135	15.828	5.332	4.712	1.00	14.88
ATOM	938	N	GLN	A	136	13.632	9.105	6.928	1.00	15.28
ATOM	939	CA	GLN	A	136	12.596	10.134	6.968	1.00	16.48
ATOM	940	C	GLN	A	136	13.102	11.418	7.646	1.00	17.46
ATOM	941	O	GLN	A	136	12.292	12.231	8.035	1.00	12.82
ATOM	942	CB	GLN	A	136	11.336	9.671	7.701	1.00	5.71
ATOM	943	CG	GLN	A	136	11.178	8.191	7.263	1.00	13.60
ATOM	944	CD	GLN	A	136	10.504	8.264	5.932	1.00	14.65
ATOM	945	OE1	GLN	A	136	9.587	9.102	5.986	1.00	23.99
ATOM	946	NE2	GLN	A	136	10.852	7.529	4.914	1.00	14.68
ATOM	947	N	ASN	A	137	14.421	11.532	7.566	1.00	18.52
ATOM	948	CA	ASN	A	137	14.953	12.752	8.141	1.00	18.16
ATOM	949	C	ASN	A	137	14.301	13.929	7.458	1.00	19.79
ATOM	950	O	ASN	A	137	13.895	14.802	8.157	1.00	12.28
ATOM	951	CB	ASN	A	137	16.481	12.573	8.239	1.00	14.17
ATOM	952	CG	ASN	A	137	17.247	13.740	8.812	1.00	19.75
ATOM	953	OD1	ASN	A	137	17.821	14.341	7.934	1.00	14.52
ATOM	954	ND2	ASN	A	137	17.390	14.130	10.042	1.00	17.43
ATOM	955	N	LEU	A	138	14.180	14.062	6.141	1.00	27.31
ATOM	956	CA	LEU	A	138	13.640	15.270	5.553	1.00	25.53
ATOM	957	C	LEU	A	138	12.190	15.332	5.971	1.00	22.45
ATOM	958	O	LEU	A	138	11.710	16.281	6.549	1.00	25.13
ATOM	959	CB	LEU	A	138	13.632	15.269	4.056	1.00	41.28

ATOM	960	CG	LEU	A	138	13.713	16.582	3.303	1.00 31.76
ATOM	961	CD1	LEU	A	138	14.641	17.503	4.012	1.00 51.09
ATOM	962	CD2	LEU	A	138	14.207	16.573	1.958	1.00 46.20
ATOM	963	N	GLN	A	139	11.378	14.403	5.569	1.00 20.48
ATOM	964	CA	GLN	A	139	10.034	14.390	6.037	1.00 19.98
ATOM	965	C	GLN	A	139	9.846	14.749	7.471	1.00 22.85
ATOM	966	O	GLN	A	139	8.791	15.282	7.528	1.00 26.66
ATOM	967	CB	GLN	A	139	9.517	12.969	5.899	1.00 18.37
ATOM	968	CG	GLN	A	139	9.684	12.643	4.450	1.00 22.02
ATOM	969	CD	GLN	A	139	10.984	11.983	4.110	1.00 22.69
ATOM	970	OE1	GLN	A	139	10.674	10.980	3.477	1.00 35.62
ATOM	971	NE2	GLN	A	139	12.195	12.405	4.410	1.00 31.70
ATOM	972	N	ASN	A	140	10.454	14.072	8.427	1.00 26.14
ATOM	973	CA	ASN	A	140	10.215	14.183	9.848	1.00 19.06
ATOM	974	C	ASN	A	140	10.941	15.429	10.293	1.00 16.99
ATOM	975	O	ASN	A	140	11.040	15.654	11.454	1.00 18.05
ATOM	976	CB	ASN	A	140	10.581	12.910	10.541	1.00 17.20
ATOM	977	CG	ASN	A	140	9.465	11.998	10.210	1.00 16.28
ATOM	978	OD1	ASN	A	140	8.615	12.565	9.563	1.00 23.57
ATOM	979	ND2	ASN	A	140	9.460	10.756	10.630	1.00 22.65
ATOM	980	N	ARG	A	141	11.457	16.162	9.397	1.00 19.20
ATOM	981	CA	ARG	A	141	12.170	17.350	9.790	1.00 26.25
ATOM	982	C	ARG	A	141	13.219	17.090	10.818	1.00 25.06
ATOM	983	O	ARG	A	141	13.365	17.928	11.649	1.00 27.60
ATOM	984	CB	ARG	A	141	11.123	18.299	10.271	1.00 37.72
ATOM	985	CG	ARG	A	141	10.083	18.974	9.372	1.00 49.61
ATOM	986	N	GLY	A	142	14.110	16.165	10.920	1.00 19.42
ATOM	987	CA	GLY	A	142	14.997	15.778	11.902	1.00 14.21
ATOM	988	C	GLY	A	142	14.652	15.066	13.158	1.00 19.42
ATOM	989	O	GLY	A	142	15.547	14.759	13.971	1.00 23.74
ATOM	990	N	GLY	A	143	13.354	14.851	13.569	1.00 14.09
ATOM	991	CA	GLY	A	143	13.210	14.075	14.757	1.00 11.80
ATOM	992	C	GLY	A	143	12.203	12.972	14.555	1.00 16.69
ATOM	993	O	GLY	A	143	11.760	12.787	13.481	1.00 19.57
ATOM	994	N	ILE	A	144	11.668	12.386	15.590	1.00 19.71
ATOM	995	CA	ILE	A	144	10.494	11.589	15.667	1.00 20.13
ATOM	996	C	ILE	A	144	9.313	12.315	16.296	1.00 27.00
ATOM	997	O	ILE	A	144	9.298	13.026	17.268	1.00 26.75
ATOM	998	CB	ILE	A	144	10.973	10.583	16.692	1.00 16.84
ATOM	999	CG1	ILE	A	144	12.363	9.956	16.348	1.00 5.60
ATOM	1000	CG2	ILE	A	144	9.882	9.636	16.775	1.00 14.01
ATOM	1001	CD1	ILE	A	144	12.437	9.156	17.562	1.00 2.75
ATOM	1002	N	PRO	A	145	8.249	12.380	15.499	1.00 32.77
ATOM	1003	CA	PRO	A	145	6.959	12.993	15.779	1.00 29.89
ATOM	1004	C	PRO	A	145	6.484	12.588	17.180	1.00 27.78
ATOM	1005	O	PRO	A	145	6.475	11.446	17.537	1.00 26.07
ATOM	1006	CB	PRO	A	145	5.957	12.384	14.784	1.00 26.51
ATOM	1007	CG	PRO	A	145	6.887	12.059	13.668	1.00 25.85

ATOM	1008	CD	PRO	A	145	8.174	11.563	14.234	1.00	31.33
ATOM	1009	N	ASN	A	146	5.796	13.462	17.878	1.00	27.07
ATOM	1010	CA	ASN	A	146	5.454	13.274	19.230	1.00	28.59
ATOM	1011	C	ASN	A	146	6.526	12.605	20.045	1.00	29.25
ATOM	1012	O	ASN	A	146	6.087	11.995	20.996	1.00	35.51
ATOM	1013	CB	ASN	A	146	4.285	12.364	19.230	1.00	41.13
ATOM	1014	CG	ASN	A	146	3.300	12.568	18.120	1.00	48.43
ATOM	1015	OD1	ASN	A	146	3.134	13.721	17.788	1.00	49.24
ATOM	1016	ND2	ASN	A	146	2.763	11.437	17.695	1.00	47.79
ATOM	1017	N	TYR	A	147	7.791	12.799	19.885	1.00	23.88
ATOM	1018	CA	TYR	A	147	8.689	12.339	20.969	1.00	21.90
ATOM	1019	C	TYR	A	147	9.583	13.495	21.285	1.00	22.57
ATOM	1020	O	TYR	A	147	9.777	14.399	20.494	1.00	26.53
ATOM	1021	CB	TYR	A	147	9.309	11.098	20.498	1.00	21.16
ATOM	1022	CG	TYR	A	147	10.285	10.471	21.349	1.00	20.45
ATOM	1023	CD1	TYR	A	147	9.882	9.720	22.384	1.00	24.28
ATOM	1024	CD2	TYR	A	147	11.608	10.564	21.189	1.00	17.96
ATOM	1025	CE1	TYR	A	147	10.681	9.029	23.273	1.00	24.55
ATOM	1026	CE2	TYR	A	147	12.509	9.948	21.983	1.00	20.73
ATOM	1027	CZ	TYR	A	147	12.022	9.184	23.030	1.00	24.61
ATOM	1028	OH	TYR	A	147	12.891	8.536	23.887	1.00	24.80
ATOM	1029	N	PRO	A	148	9.893	13.858	22.507	1.00	22.86
ATOM	1030	CA	PRO	A	148	10.817	14.916	22.769	1.00	21.77
ATOM	1031	C	PRO	A	148	12.127	14.882	21.957	1.00	22.49
ATOM	1032	O	PRO	A	148	13.007	14.004	22.117	1.00	22.31
ATOM	1033	CB	PRO	A	148	11.185	14.694	24.251	1.00	23.23
ATOM	1034	CG	PRO	A	148	10.324	13.576	24.719	1.00	23.39
ATOM	1035	CD	PRO	A	148	9.677	12.889	23.590	1.00	25.33
ATOM	1036	N	ARG	A	149	12.432	15.980	21.250	1.00	25.45
ATOM	1037	CA	ARG	A	149	13.735	16.138	20.567	1.00	22.54
ATOM	1038	C	ARG	A	149	14.910	16.018	21.499	1.00	21.28
ATOM	1039	O	ARG	A	149	15.860	15.477	21.015	1.00	16.61
ATOM	1040	CB	ARG	A	149	13.829	17.346	19.727	1.00	31.02
ATOM	1041	CG	ARG	A	149	12.837	17.750	18.719	1.00	58.26
ATOM	1042	CD	ARG	A	149	13.452	18.605	17.658	1.00	80.58
ATOM	1043	NE	ARG	A	149	13.769	17.798	16.491	1.00	92.05
ATOM	1044	CZ	ARG	A	149	13.315	18.154	15.320	1.00	91.85
ATOM	1045	NH1	ARG	A	149	12.586	19.213	15.165	1.00	86.98
ATOM	1046	NH2	ARG	A	149	13.544	17.488	14.242	1.00	91.61
ATOM	1047	N	GLU	A	150	14.813	16.282	22.825	1.00	28.09
ATOM	1048	CA	GLU	A	150	15.950	16.171	23.735	1.00	25.55
ATOM	1049	C	GLU	A	150	16.272	14.736	24.020	1.00	21.12
ATOM	1050	O	GLU	A	150	17.372	14.443	24.371	1.00	24.39
ATOM	1051	CB	GLU	A	150	15.753	17.040	24.917	1.00	38.73
ATOM	1052	CG	GLU	A	150	14.328	17.370	25.359	1.00	67.27
ATOM	1053	CD	GLU	A	150	14.252	17.185	26.899	1.00	85.05
ATOM	1054	OE1	GLU	A	150	15.005	17.890	27.657	1.00	90.70
ATOM	1055	OE2	GLU	A	150	13.454	16.321	27.373	1.00	91.68

ATOM	1056	N	ARG	A	151	15.396	13.807	23.727	1.00	19.70
ATOM	1057	CA	ARG	A	151	15.752	12.424	23.844	1.00	19.52
ATOM	1058	C	ARG	A	151	16.163	11.779	22.531	1.00	19.28
ATOM	1059	O	ARG	A	151	16.373	10.586	22.480	1.00	14.55
ATOM	1060	CB	ARG	A	151	14.548	11.796	24.412	1.00	23.06
ATOM	1061	CG	ARG	A	151	13.853	12.432	25.516	1.00	22.24
ATOM	1062	CD	ARG	A	151	13.200	11.451	26.393	1.00	33.40
ATOM	1063	NE	ARG	A	151	12.609	11.893	27.633	1.00	46.53
ATOM	1064	CZ	ARG	A	151	11.796	11.028	28.275	1.00	52.87
ATOM	1065	NH1	ARG	A	151	11.428	9.823	27.930	1.00	51.02
ATOM	1066	NH2	ARG	A	151	11.203	11.278	29.416	1.00	59.98
ATOM	1067	N	THR	A	152	16.360	12.526	21.505	1.00	14.12
ATOM	1068	CA	THR	A	152	16.629	11.925	20.253	1.00	15.05
ATOM	1069	C	THR	A	152	17.995	12.249	19.745	1.00	17.30
ATOM	1070	O	THR	A	152	18.282	13.373	19.965	1.00	21.34
ATOM	1071	CB	THR	A	152	15.680	12.408	19.158	1.00	13.91
ATOM	1072	OG1	THR	A	152	14.423	12.256	19.858	1.00	23.92
ATOM	1073	CG2	THR	A	152	15.737	11.934	17.759	1.00	6.77
ATOM	1074	N	LYS	A	153	18.704	11.336	19.121	1.00	15.49
ATOM	1075	CA	LYS	A	153	19.930	11.725	18.450	1.00	17.73
ATOM	1076	C	LYS	A	153	19.893	11.035	17.073	1.00	18.41
ATOM	1077	O	LYS	A	153	19.866	9.800	17.121	1.00	16.04
ATOM	1078	CB	LYS	A	153	21.112	11.260	19.338	1.00	14.55
ATOM	1079	CG	LYS	A	153	22.523	11.508	18.933	1.00	11.95
ATOM	1080	CD	LYS	A	153	22.883	12.882	19.403	1.00	40.35
ATOM	1081	CE	LYS	A	153	24.358	13.093	19.079	1.00	62.12
ATOM	1082	NZ	LYS	A	153	24.930	14.235	19.863	1.00	73.03
ATOM	1083	N	VAL	A	154	19.910	11.962	16.136	1.00	15.86
ATOM	1084	CA	VAL	A	154	20.031	11.508	14.730	1.00	15.79
ATOM	1085	C	VAL	A	154	21.406	11.481	14.040	1.00	13.11
ATOM	1086	O	VAL	A	154	21.958	12.460	13.675	1.00	13.51
ATOM	1087	CB	VAL	A	154	19.095	12.257	13.674	1.00	5.90
ATOM	1088	CG1	VAL	A	154	19.276	11.765	12.247	1.00	8.45
ATOM	1089	CG2	VAL	A	154	17.672	12.091	14.117	1.00	7.14
ATOM	1090	N	PHE	A	155	22.039	10.448	13.605	1.00	13.75
ATOM	1091	CA	PHE	A	155	23.263	10.473	12.843	1.00	10.67
ATOM	1092	C	PHE	A	155	22.906	10.406	11.402	1.00	11.64
ATOM	1093	O	PHE	A	155	22.505	9.367	10.893	1.00	15.09
ATOM	1094	CB	PHE	A	155	23.955	9.120	13.304	1.00	5.38
ATOM	1095	CG	PHE	A	155	24.396	9.266	14.739	1.00	16.52
ATOM	1096	CD1	PHE	A	155	23.678	8.642	15.696	1.00	23.70
ATOM	1097	CD2	PHE	A	155	25.503	9.950	15.107	1.00	11.27
ATOM	1098	CE1	PHE	A	155	24.037	8.702	17.011	1.00	23.25
ATOM	1099	CE2	PHE	A	155	25.888	9.994	16.372	1.00	7.37
ATOM	1100	CZ	PHE	A	155	25.139	9.384	17.357	1.00	16.13
ATOM	1101	N	CYS	A	156	23.205	11.255	10.511	1.00	12.38
ATOM	1102	CA	CYS	A	156	22.847	11.443	9.114	1.00	11.64
ATOM	1103	C	CYS	A	156	24.057	12.027	8.461	1.00	10.08

ATOM	1104	O	CYS	A	156	24.385	13.174	8.378	1.00	13.73
ATOM	1105	CB	CYS	A	156	21.575	12.391	8.917	1.00	6.30
ATOM	1106	SG	CYS	A	156	20.137	11.470	8.287	1.00	10.60
ATOM	1107	N	ASN	A	157	24.814	11.147	7.918	1.00	16.95
ATOM	1108	CA	ASN	A	157	26.229	11.665	7.576	1.00	19.16
ATOM	1109	C	ASN	A	157	26.197	12.367	6.310	1.00	17.70
ATOM	1110	O	ASN	A	157	25.368	12.330	5.469	1.00	20.91
ATOM	1111	CB	ASN	A	157	27.115	10.714	8.300	1.00	30.34
ATOM	1112	CG	ASN	A	157	27.733	9.498	7.932	1.00	34.95
ATOM	1113	OD1	ASN	A	157	28.011	8.573	8.606	1.00	44.28
ATOM	1114	ND2	ASN	A	157	27.965	9.541	6.660	1.00	54.18
ATOM	1115	N	VAL	A	158	26.849	13.501	6.313	1.00	25.65
ATOM	1116	CA	VAL	A	158	26.825	14.483	5.192	1.00	28.21
ATOM	1117	C	VAL	A	158	26.768	13.893	3.758	1.00	24.85
ATOM	1118	O	VAL	A	158	25.732	14.266	3.111	1.00	30.96
ATOM	1119	CB	VAL	A	158	27.954	15.512	5.217	1.00	27.87
ATOM	1120	CG1	VAL	A	158	28.751	14.595	4.238	1.00	40.51
ATOM	1121	CG2	VAL	A	158	27.791	16.704	4.399	1.00	34.39
ATOM	1122	N	GLY	A	159	27.483	12.956	3.016	1.00	5.94
ATOM	1123	CA	GLY	A	159	26.713	12.774	1.732	1.00	6.20
ATOM	1124	C	GLY	A	159	25.734	11.797	1.487	1.00	4.00
ATOM	1125	O	GLY	A	159	25.732	10.704	0.848	1.00	4.06
ATOM	1126	N	ASP	A	160	25.052	11.441	2.643	1.00	8.53
ATOM	1127	CA	ASP	A	160	24.106	10.302	2.828	1.00	11.97
ATOM	1128	C	ASP	A	160	22.755	10.698	2.177	1.00	14.44
ATOM	1129	O	ASP	A	160	21.928	11.398	2.692	1.00	10.21
ATOM	1130	CB	ASP	A	160	24.037	9.829	4.277	1.00	12.43
ATOM	1131	CG	ASP	A	160	23.126	8.629	4.261	1.00	20.99
ATOM	1132	OD1	ASP	A	160	22.525	8.408	3.179	1.00	33.03
ATOM	1133	OD2	ASP	A	160	22.956	7.840	5.216	1.00	10.13
ATOM	1134	N	ALA	A	161	22.455	10.402	0.961	1.00	12.33
ATOM	1135	CA	ALA	A	161	21.318	10.743	0.269	1.00	11.01
ATOM	1136	C	ALA	A	161	19.961	10.317	0.848	1.00	15.22
ATOM	1137	O	ALA	A	161	18.969	11.034	0.594	1.00	9.50
ATOM	1138	CB	ALA	A	161	21.365	10.334	-1.172	1.00	13.68
ATOM	1139	N	VAL	A	162	19.915	9.468	1.840	1.00	14.54
ATOM	1140	CA	VAL	A	162	18.653	9.014	2.287	1.00	9.86
ATOM	1141	C	VAL	A	162	18.235	10.063	3.258	1.00	13.50
ATOM	1142	O	VAL	A	162	17.094	10.458	3.377	1.00	20.47
ATOM	1143	CB	VAL	A	162	18.596	7.778	3.117	1.00	7.34
ATOM	1144	CG1	VAL	A	162	18.931	6.592	2.259	1.00	6.50
ATOM	1145	CG2	VAL	A	162	19.514	7.858	4.210	1.00	18.46
ATOM	1146	N	CYS	A	163	19.198	10.733	3.719	1.00	13.44
ATOM	1147	CA	CYS	A	163	18.864	11.811	4.720	1.00	11.26
ATOM	1148	C	CYS	A	163	18.256	12.963	4.042	1.00	15.57
ATOM	1149	O	CYS	A	163	18.219	13.857	4.880	1.00	14.09
ATOM	1150	CB	CYS	A	163	20.144	12.145	5.570	1.00	18.70
ATOM	1151	SG	CYS	A	163	20.748	10.705	6.581	1.00	13.38

ATOM	1152	N	THR	A	164	18.100	13.014	2.696	1.00	21.82
ATOM	1153	CA	THR	A	164	17.603	14.283	2.171	1.00	23.08
ATOM	1154	C	THR	A	164	16.597	14.022	1.098	1.00	23.39
ATOM	1155	O	THR	A	164	16.517	14.727	0.137	1.00	33.37
ATOM	1156	CB	THR	A	164	18.463	15.341	1.454	1.00	23.25
ATOM	1157	OG1	THR	A	164	19.486	14.707	0.674	1.00	23.21
ATOM	1158	CG2	THR	A	164	18.958	16.261	2.491	1.00	37.71
ATOM	1159	N	GLY	A	165	15.802	13.085	1.309	1.00	24.23
ATOM	1160	CA	GLY	A	165	14.606	12.783	0.579	1.00	26.69
ATOM	1161	C	GLY	A	165	14.699	11.814	-0.515	1.00	28.56
ATOM	1162	O	GLY	A	165	13.680	11.775	-1.124	1.00	39.76
ATOM	1163	N	THR	A	166	15.661	11.044	-0.736	1.00	25.80
ATOM	1164	CA	THR	A	166	16.006	10.220	-1.774	1.00	25.53
ATOM	1165	C	THR	A	166	16.195	8.866	-1.175	1.00	25.35
ATOM	1166	O	THR	A	166	16.913	8.760	-0.206	1.00	30.91
ATOM	1167	CB	THR	A	166	17.406	10.657	-2.230	1.00	31.57
ATOM	1168	OG1	THR	A	166	17.105	11.788	-2.982	1.00	24.13
ATOM	1169	CG2	THR	A	166	18.061	9.559	-2.983	1.00	34.67
ATOM	1170	N	LEU	A	167	15.734	7.833	-1.817	1.00	19.63
ATOM	1171	CA	LEU	A	167	16.219	6.552	-1.465	1.00	16.11
ATOM	1172	C	LEU	A	167	17.395	6.044	-2.300	1.00	19.87
ATOM	1173	O	LEU	A	167	17.265	4.869	-2.612	1.00	21.38
ATOM	1174	CB	LEU	A	167	15.086	5.624	-1.555	1.00	23.45
ATOM	1175	CG	LEU	A	167	14.123	5.773	-0.401	1.00	33.91
ATOM	1176	CD1	LEU	A	167	12.969	4.908	-0.793	1.00	42.10
ATOM	1177	CD2	LEU	A	167	14.776	5.385	0.903	1.00	25.86
ATOM	1178	N	ILE	A	168	18.534	6.726	-2.507	1.00	21.67
ATOM	1179	CA	ILE	A	168	19.608	6.051	-3.170	1.00	23.38
ATOM	1180	C	ILE	A	168	20.675	5.585	-2.189	1.00	20.47
ATOM	1181	O	ILE	A	168	21.139	6.541	-1.581	1.00	18.08
ATOM	1182	CB	ILE	A	168	20.254	6.835	-4.297	1.00	23.50
ATOM	1183	CG1	ILE	A	168	21.232	7.874	-3.800	1.00	13.71
ATOM	1184	CG2	ILE	A	168	19.445	7.627	-5.276	1.00	18.16
ATOM	1185	CD1	ILE	A	168	20.908	8.938	-4.804	1.00	26.95
ATOM	1186	N	ILE	A	169	21.396	4.478	-2.394	1.00	18.32
ATOM	1187	CA	ILE	A	169	22.554	4.448	-1.536	1.00	13.25
ATOM	1188	C	ILE	A	169	23.924	4.662	-1.967	1.00	11.95
ATOM	1189	O	ILE	A	169	24.615	3.942	-2.539	1.00	20.35
ATOM	1190	CB	ILE	A	169	22.503	3.351	-0.499	1.00	21.07
ATOM	1191	CG1	ILE	A	169	23.398	2.181	-0.655	1.00	11.06
ATOM	1192	CG2	ILE	A	169	21.122	2.801	-0.533	1.00	7.02
ATOM	1193	CD1	ILE	A	169	22.581	1.266	-1.587	1.00	32.83
ATOM	1194	N	THR	A	170	24.570	5.586	-1.296	1.00	17.16
ATOM	1195	CA	THR	A	170	25.883	6.217	-1.397	1.00	13.01
ATOM	1196	C	THR	A	170	26.722	5.719	-0.240	1.00	10.14
ATOM	1197	O	THR	A	170	26.334	5.036	0.758	1.00	9.98
ATOM	1198	CB	THR	A	170	25.623	7.713	-1.344	1.00	15.02
ATOM	1199	OG1	THR	A	170	26.466	7.947	-0.255	1.00	23.39

ATOM	1200	CG2	THR	A	170	24.389	7.914	-0.452	1.00	41.10
ATOM	1201	N	PRO	A	171	28.000	5.738	-0.469	1.00	10.12
ATOM	1202	CA	PRO	A	171	29.012	5.066	0.339	1.00	11.88
ATOM	1203	C	PRO	A	171	28.897	5.492	1.765	1.00	9.74
ATOM	1204	O	PRO	A	171	28.904	4.682	2.646	1.00	9.54
ATOM	1205	CB	PRO	A	171	30.414	5.207	-0.286	1.00	7.15
ATOM	1206	CG	PRO	A	171	30.017	5.603	-1.654	1.00	7.18
ATOM	1207	CD	PRO	A	171	28.667	6.233	-1.601	1.00	6.90
ATOM	1208	N	ALA	A	172	28.725	6.718	1.980	1.00	6.71
ATOM	1209	CA	ALA	A	172	28.247	7.315	3.169	1.00	8.62
ATOM	1210	C	ALA	A	172	27.075	6.631	3.892	1.00	10.99
ATOM	1211	O	ALA	A	172	27.037	6.755	5.165	1.00	16.49
ATOM	1212	CB	ALA	A	172	27.904	8.812	3.040	1.00	2.86
ATOM	1213	N	HIS	A	173	26.287	5.815	3.278	1.00	6.36
ATOM	1214	CA	HIS	A	173	25.133	5.468	4.081	1.00	5.29
ATOM	1215	C	HIS	A	173	25.685	4.314	4.888	1.00	10.58
ATOM	1216	O	HIS	A	173	25.082	3.598	5.668	1.00	9.36
ATOM	1217	CB	HIS	A	173	24.081	4.883	3.216	1.00	8.41
ATOM	1218	CG	HIS	A	173	22.815	4.403	3.791	1.00	7.30
ATOM	1219	ND1	HIS	A	173	22.066	5.327	4.565	1.00	8.48
ATOM	1220	CD2	HIS	A	173	22.148	3.264	3.670	1.00	7.83
ATOM	1221	CE1	HIS	A	173	20.932	4.657	4.861	1.00	17.36
ATOM	1222	NE2	HIS	A	173	20.945	3.423	4.379	1.00	5.29
ATOM	1223	N	LEU	A	174	26.823	3.947	4.326	1.00	8.03
ATOM	1224	CA	LEU	A	174	27.344	2.623	4.682	1.00	8.06
ATOM	1225	C	LEU	A	174	28.171	2.787	5.930	1.00	13.06
ATOM	1226	O	LEU	A	174	28.609	1.648	6.151	1.00	19.88
ATOM	1227	CB	LEU	A	174	28.078	2.118	3.488	1.00	2.76
ATOM	1228	CG	LEU	A	174	27.560	0.902	2.847	1.00	13.35
ATOM	1229	CD1	LEU	A	174	26.024	1.017	2.796	1.00	18.01
ATOM	1230	CD2	LEU	A	174	27.913	0.740	1.421	1.00	21.70
ATOM	1231	N	SER	A	175	28.290	3.989	6.447	1.00	12.43
ATOM	1232	CA	SER	A	175	29.230	4.052	7.553	1.00	18.01
ATOM	1233	C	SER	A	175	28.872	4.811	8.847	1.00	19.89
ATOM	1234	O	SER	A	175	28.968	6.047	9.120	1.00	14.61
ATOM	1235	CB	SER	A	175	30.516	4.606	6.847	1.00	20.11
ATOM	1236	OG	SER	A	175	30.834	5.907	7.293	1.00	27.73
ATOM	1237	N	TYR	A	176	28.479	3.978	9.815	1.00	17.89
ATOM	1238	CA	TYR	A	176	28.092	4.530	11.133	1.00	12.54
ATOM	1239	C	TYR	A	176	28.530	3.671	12.272	1.00	11.16
ATOM	1240	O	TYR	A	176	27.949	3.770	13.257	1.00	7.63
ATOM	1241	CB	TYR	A	176	26.511	4.283	11.053	1.00	9.13
ATOM	1242	CG	TYR	A	176	25.831	5.525	10.029	1.00	5.03
ATOM	1243	CD1	TYR	A	176	25.874	6.923	10.425	1.00	2.75
ATOM	1244	CD2	TYR	A	176	25.152	5.022	8.980	1.00	2.18
ATOM	1245	CE1	TYR	A	176	25.287	7.754	9.633	1.00	4.25
ATOM	1246	CE2	TYR	A	176	24.649	5.981	8.085	1.00	6.77
ATOM	1247	CZ	TYR	A	176	24.658	7.329	8.399	1.00	6.22

ATOM	1248	OH	TYR	A	176	24.074	8.375	7.635	1.00	5.76
ATOM	1249	N	THR	A	177	29.430	2.685	12.167	1.00	10.72
ATOM	1250	CA	THR	A	177	29.797	1.854	13.284	1.00	13.31
ATOM	1251	C	THR	A	177	30.516	2.659	14.320	1.00	12.46
ATOM	1252	O	THR	A	177	30.311	2.436	15.475	1.00	13.12
ATOM	1253	CB	THR	A	177	30.658	0.683	12.798	1.00	3.49
ATOM	1254	OG1	THR	A	177	31.361	1.247	11.870	1.00	32.08
ATOM	1255	CG2	THR	A	177	29.675	-0.149	12.083	1.00	6.42
ATOM	1256	N	ILE	A	178	31.409	3.474	13.920	1.00	10.48
ATOM	1257	CA	ILE	A	178	32.203	4.246	14.783	1.00	15.25
ATOM	1258	C	ILE	A	178	31.180	5.045	15.632	1.00	16.95
ATOM	1259	O	ILE	A	178	31.092	4.774	16.851	1.00	22.68
ATOM	1260	CB	ILE	A	178	33.338	5.121	14.357	1.00	25.11
ATOM	1261	CG1	ILE	A	178	34.701	4.496	14.056	1.00	25.05
ATOM	1262	CG2	ILE	A	178	33.599	6.205	15.392	1.00	27.60
ATOM	1263	CD1	ILE	A	178	34.553	3.006	14.071	1.00	55.86
ATOM	1264	N	GLU	A	179	30.218	5.799	15.178	1.00	16.34
ATOM	1265	CA	GLU	A	179	29.290	6.610	15.985	1.00	16.94
ATOM	1266	C	GLU	A	179	28.324	5.713	16.692	1.00	14.79
ATOM	1267	O	GLU	A	179	27.683	6.012	17.716	1.00	19.20
ATOM	1268	CB	GLU	A	179	28.555	7.637	15.169	1.00	21.16
ATOM	1269	CG	GLU	A	179	28.790	7.283	13.691	1.00	50.37
ATOM	1270	CD	GLU	A	179	29.933	7.701	12.851	1.00	61.82
ATOM	1271	OE1	GLU	A	179	30.163	8.890	12.697	1.00	77.56
ATOM	1272	OE2	GLU	A	179	30.627	6.854	12.309	1.00	75.83
ATOM	1273	N	ALA	A	180	28.240	4.418	16.412	1.00	8.00
ATOM	1274	CA	ALA	A	180	27.353	3.520	17.042	1.00	14.34
ATOM	1275	C	ALA	A	180	28.048	2.991	18.280	1.00	19.53
ATOM	1276	O	ALA	A	180	27.397	3.142	19.265	1.00	21.17
ATOM	1277	CB	ALA	A	180	26.843	2.437	16.128	1.00	11.97
ATOM	1278	N	ARG	A	181	29.317	2.547	18.287	1.00	21.89
ATOM	1279	CA	ARG	A	181	29.992	1.982	19.398	1.00	16.48
ATOM	1280	C	ARG	A	181	30.296	3.106	20.367	1.00	19.44
ATOM	1281	O	ARG	A	181	30.243	3.104	21.639	1.00	28.53
ATOM	1282	CB	ARG	A	181	31.310	1.408	19.143	1.00	12.43
ATOM	1283	CG	ARG	A	181	31.954	0.432	20.052	1.00	45.44
ATOM	1284	CD	ARG	A	181	32.596	-0.688	19.242	1.00	66.21
ATOM	1285	NE	ARG	A	181	33.333	-0.030	18.164	1.00	85.83
ATOM	1286	CZ	ARG	A	181	33.306	-0.321	16.895	1.00	91.35
ATOM	1287	NH1	ARG	A	181	32.551	-1.320	16.530	1.00	96.98
ATOM	1288	NH2	ARG	A	181	34.023	0.400	16.095	1.00	92.83
ATOM	1289	N	GLY	A	182	30.387	4.262	19.847	1.00	13.94
ATOM	1290	CA	GLY	A	182	30.553	5.404	20.728	1.00	7.40
ATOM	1291	C	GLY	A	182	29.741	6.574	20.960	1.00	7.95
ATOM	1292	O	GLY	A	182	29.171	6.512	22.083	1.00	12.73
ATOM	1293	N	GLU	A	183	29.725	7.622	20.138	1.00	6.42
ATOM	1294	CA	GLU	A	183	28.816	8.775	20.405	1.00	10.04
ATOM	1295	C	GLU	A	183	27.421	8.369	20.645	1.00	14.41

ATOM	1296	O	GLU	A	183	26.846	8.530	21.749	1.00	15.43
ATOM	1297	CB	GLU	A	183	29.053	9.791	19.402	1.00	21.24
ATOM	1298	CG	GLU	A	183	28.079	10.638	18.725	1.00	62.21
ATOM	1299	CD	GLU	A	183	28.248	12.103	19.141	1.00	81.34
ATOM	1300	OE1	GLU	A	183	28.850	12.243	20.232	1.00	95.85
ATOM	1301	OE2	GLU	A	183	27.791	13.027	18.430	1.00	90.85
ATOM	1302	N	ALA	A	184	26.766	7.605	19.808	1.00	15.56
ATOM	1303	CA	ALA	A	184	25.444	7.083	20.117	1.00	14.54
ATOM	1304	C	ALA	A	184	25.549	6.382	21.464	1.00	13.62
ATOM	1305	O	ALA	A	184	24.575	6.533	22.215	1.00	16.75
ATOM	1306	CB	ALA	A	184	25.019	6.015	19.089	1.00	9.58
ATOM	1307	N	ALA	A	185	26.428	5.396	21.774	1.00	9.42
ATOM	1308	CA	ALA	A	185	26.219	4.677	23.031	1.00	7.48
ATOM	1309	C	ALA	A	185	26.330	5.715	24.100	1.00	12.30
ATOM	1310	O	ALA	A	185	25.761	5.503	25.179	1.00	9.50
ATOM	1311	CB	ALA	A	185	27.138	3.475	23.260	1.00	4.60
ATOM	1312	N	ARG	A	186	27.271	6.673	24.090	1.00	15.54
ATOM	1313	CA	ARG	A	186	27.352	7.507	25.300	1.00	13.57
ATOM	1314	C	ARG	A	186	26.085	8.286	25.561	1.00	11.49
ATOM	1315	O	ARG	A	186	25.421	8.267	26.573	1.00	8.74
ATOM	1316	CB	ARG	A	186	28.484	8.460	25.043	1.00	30.29
ATOM	1317	CG	ARG	A	186	29.869	7.851	25.240	1.00	37.15
ATOM	1318	CD	ARG	A	186	30.983	8.826	24.813	1.00	42.36
ATOM	1319	NE	ARG	A	186	31.902	7.942	24.064	1.00	51.82
ATOM	1320	CZ	ARG	A	186	32.324	8.346	22.870	1.00	50.20
ATOM	1321	NH1	ARG	A	186	31.924	9.538	22.424	1.00	47.65
ATOM	1322	NH2	ARG	A	186	33.115	7.476	22.318	1.00	39.90
ATOM	1323	N	PHE	A	187	25.565	8.774	24.434	1.00	8.37
ATOM	1324	CA	PHE	A	187	24.195	9.370	24.426	1.00	13.48
ATOM	1325	C	PHE	A	187	23.187	8.476	25.182	1.00	15.92
ATOM	1326	O	PHE	A	187	22.379	8.916	25.995	1.00	14.81
ATOM	1327	CB	PHE	A	187	23.667	9.791	23.087	1.00	11.81
ATOM	1328	CG	PHE	A	187	22.282	10.323	23.032	1.00	14.64
ATOM	1329	CD1	PHE	A	187	21.984	11.586	23.391	1.00	8.47
ATOM	1330	CD2	PHE	A	187	21.186	9.599	22.564	1.00	18.34
ATOM	1331	CE1	PHE	A	187	20.698	12.134	23.353	1.00	12.89
ATOM	1332	CE2	PHE	A	187	19.895	10.026	22.485	1.00	17.42
ATOM	1333	CZ	PHE	A	187	19.661	11.322	22.924	1.00	3.70
ATOM	1334	N	LEU	A	188	23.033	7.232	24.803	1.00	15.17
ATOM	1335	CA	LEU	A	188	21.908	6.427	25.324	1.00	18.43
ATOM	1336	C	LEU	A	188	22.207	6.221	26.775	1.00	19.67
ATOM	1337	O	LEU	A	188	21.280	6.512	27.461	1.00	18.17
ATOM	1338	CB	LEU	A	188	21.703	5.088	24.552	1.00	18.72
ATOM	1339	CG	LEU	A	188	21.116	5.375	23.136	1.00	9.96
ATOM	1340	CD1	LEU	A	188	20.950	4.066	22.601	1.00	7.86
ATOM	1341	CD2	LEU	A	188	19.849	6.206	23.168	1.00	4.70
ATOM	1342	N	ARG	A	189	23.333	5.805	27.230	1.00	17.48
ATOM	1343	CA	ARG	A	189	23.798	5.812	28.547	1.00	18.41

ATOM	1344	C	ARG	A	189	23.353	7.039	29.321	1.00 16.87
ATOM	1345	O	ARG	A	189	22.852	7.164	30.389	1.00 13.64
ATOM	1346	CB	ARG	A	189	25.325	6.017	28.529	1.00 21.93
ATOM	1347	CG	ARG	A	189	25.882	5.624	29.894	1.00 19.95
ATOM	1348	CD	ARG	A	189	27.239	6.140	30.235	1.00 21.42
ATOM	1349	NE	ARG	A	189	27.257	7.545	29.926	1.00 25.62
ATOM	1350	CZ	ARG	A	189	28.491	7.983	29.699	1.00 29.22
ATOM	1351	NH1	ARG	A	189	29.315	6.960	29.840	1.00 26.71
ATOM	1352	NH2	ARG	A	189	28.780	9.210	29.383	1.00 33.27
ATOM	1353	N	ASP	A	190	23.837	8.150	28.796	1.00 13.76
ATOM	1354	CA	ASP	A	190	23.489	9.338	29.615	1.00 17.78
ATOM	1355	C	ASP	A	190	22.008	9.364	29.711	1.00 16.79
ATOM	1356	O	ASP	A	190	21.661	9.891	30.692	1.00 23.13
ATOM	1357	CB	ASP	A	190	23.995	10.663	29.070	1.00 23.17
ATOM	1358	CG	ASP	A	190	25.553	10.664	29.079	1.00 33.40
ATOM	1359	OD1	ASP	A	190	26.250	9.836	29.761	1.00 22.68
ATOM	1360	OD2	ASP	A	190	25.961	11.595	28.321	1.00 30.24
ATOM	1361	N	ARG	A	191	21.156	9.128	28.781	1.00 21.61
ATOM	1362	CA	ARG	A	191	19.707	9.265	28.849	1.00 20.99
ATOM	1363	C	ARG	A	191	19.176	8.237	29.825	1.00 21.23
ATOM	1364	O	ARG	A	191	18.327	8.515	30.651	1.00 20.98
ATOM	1365	CB	ARG	A	191	19.014	9.214	27.450	1.00 19.76
ATOM	1366	CG	ARG	A	191	19.605	10.282	26.521	1.00 27.49
ATOM	1367	CD	ARG	A	191	18.848	11.594	26.689	1.00 36.68
ATOM	1368	NE	ARG	A	191	17.559	11.023	27.144	1.00 60.89
ATOM	1369	CZ	ARG	A	191	16.841	11.651	28.087	1.00 73.30
ATOM	1370	NH1	ARG	A	191	17.404	12.780	28.496	1.00 76.65
ATOM	1371	NH2	ARG	A	191	15.675	11.224	28.574	1.00 62.02
ATOM	1372	N	ILE	A	192	19.734	7.037	29.885	1.00 21.02
ATOM	1373	CA	ILE	A	192	19.500	6.080	30.913	1.00 21.92
ATOM	1374	C	ILE	A	192	19.705	6.598	32.337	1.00 25.67
ATOM	1375	O	ILE	A	192	19.145	6.053	33.263	1.00 27.95
ATOM	1376	CB	ILE	A	192	20.289	4.775	30.750	1.00 24.23
ATOM	1377	CG1	ILE	A	192	19.770	4.215	29.475	1.00 26.91
ATOM	1378	CG2	ILE	A	192	19.923	3.983	31.951	1.00 15.15
ATOM	1379	CD1	ILE	A	192	20.418	2.954	29.019	1.00 21.07
ATOM	1380	N	ARG	A	193	20.535	7.574	32.629	1.00 28.72
ATOM	1381	CA	ARG	A	193	20.800	8.068	33.963	1.00 33.95
ATOM	1382	C	ARG	A	193	20.116	9.377	34.406	1.00 42.87
ATOM	1383	O	ARG	A	193	20.479	9.267	35.618	1.00 48.19
ATOM	1384	CB	ARG	A	193	22.298	8.179	34.167	1.00 34.19
ATOM	1385	CG	ARG	A	193	23.096	6.896	34.100	1.00 39.38
ATOM	1386	CD	ARG	A	193	24.590	7.213	34.133	1.00 65.92
ATOM	1387	NE	ARG	A	193	25.339	5.973	34.003	1.00 81.05
ATOM	1388	CZ	ARG	A	193	26.631	5.765	33.770	1.00 81.52
ATOM	1389	NH1	ARG	A	193	27.441	6.816	33.647	1.00 80.92
ATOM	1390	NH2	ARG	A	193	27.120	4.536	33.652	1.00 74.00
ATOM	1391	OT	ARG	A	193	19.292	10.277	34.082	1.00 38.80
TER									

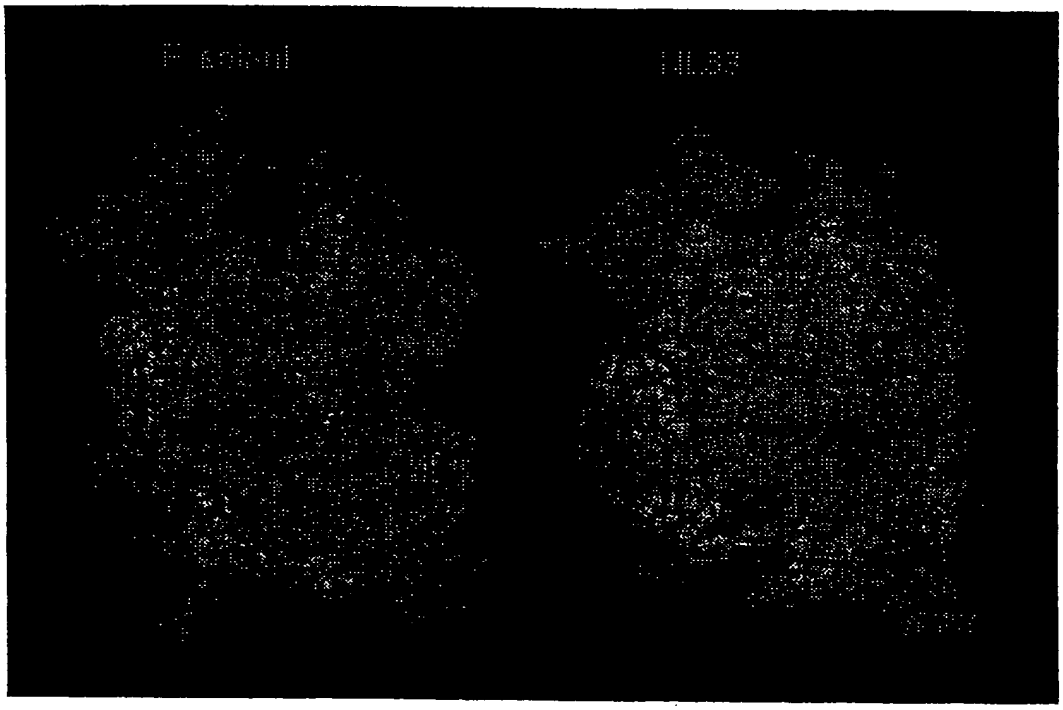

Fig. 2

3D structure of cutinases from *F. solani pisi* (left) and *H. insolens* (right)

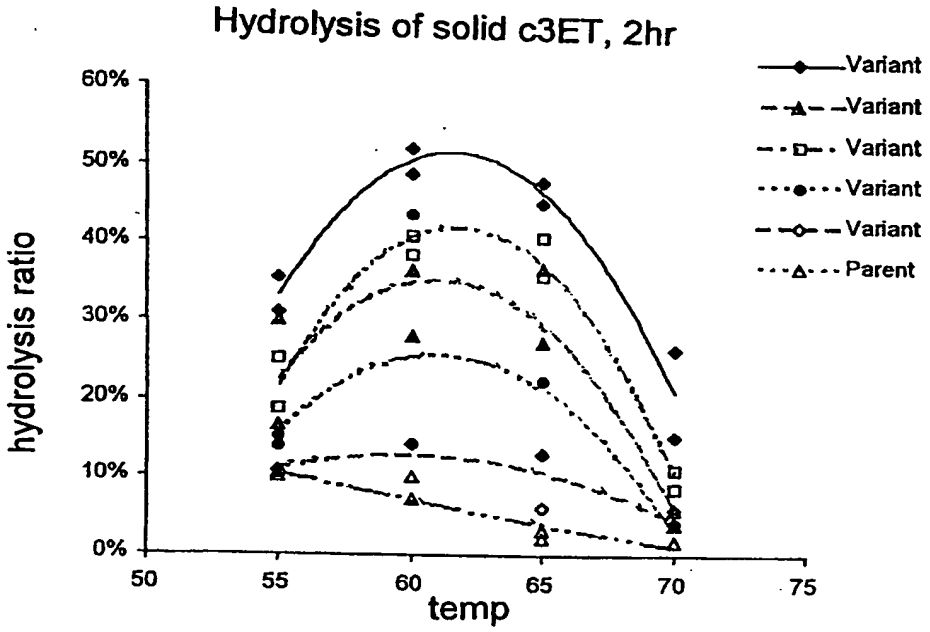

Fig. 3

Hydrolysis of solid c3ET, 2 hr

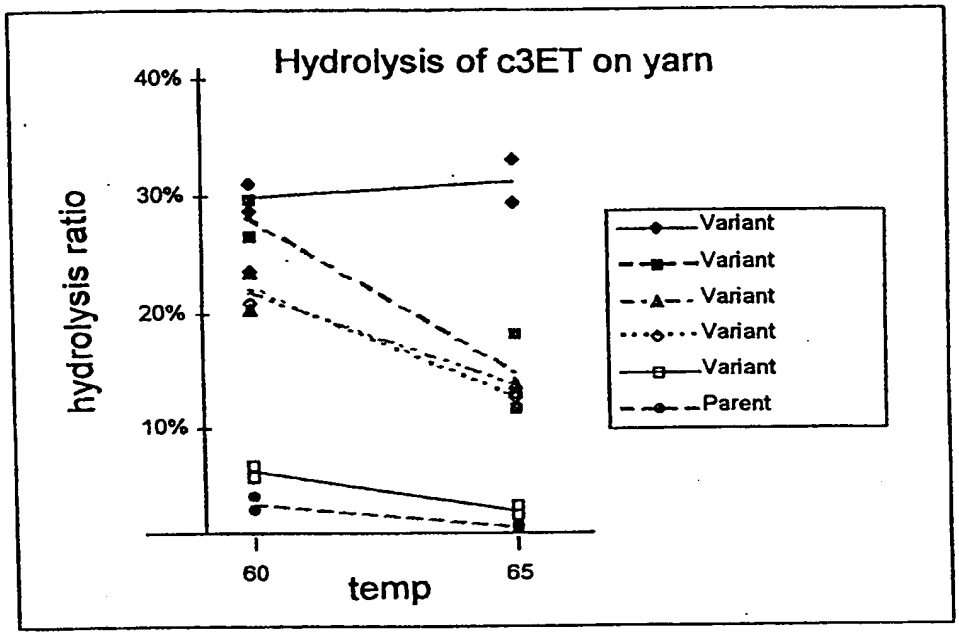

Fig. 4

Hydrolysis of c3ET on yarn, 17 hr

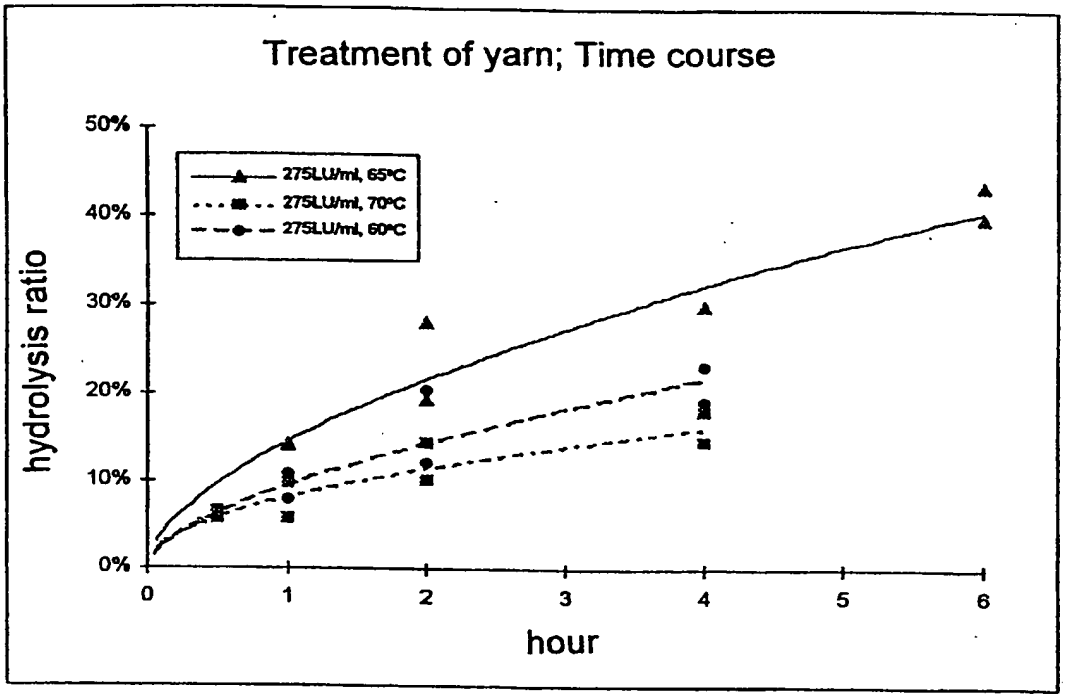

Fig. 5

Treatment of yarn; time course

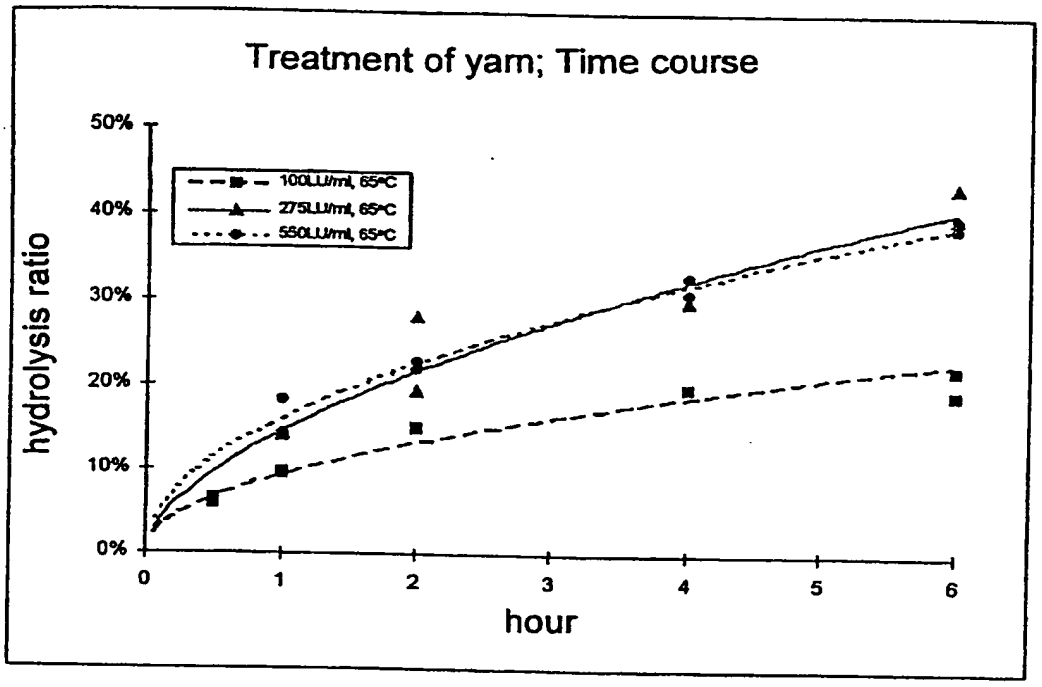

Fig. 6

Treatment of yarn; time course

INTERNATIONAL SEARCH REPORT

International application No.
PCT/DK 99/00678

A. CLASSIFICATION OF SUBJECT MATTER

IPC7: C12N 9/18 // C11D 3/386, C08G 63/91
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC7: C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

SE,DK,FI,NO classes as above

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 9009446 A1 (PLANT GENETICS SYSTEMS, N.V.), 23 August 1990 (23.08.90), see page 1, lines 11-20, claims	1-32,34
X	WO 9414963 A1 (UNILEVER N.V.), 7 July 1994 (07.07.94), see claim 14	1-32,34
A	WO 9414964 A1 (UNILEVER N.V.), 7 July 1994 (07.07.94)	1-32,34
A	WO 9704078 A1 (NOVO NORDISK A/S), 6 February 1997 (06.02.97), see claim 51	1-32,34

[X] Further documents are listed in the continuation of Box C. [X] See patent family annex.

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" erlier document but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
8 May 2000	11 -05- 2000
Name and mailing address of the ISA/ Swedish Patent Office Box 5055, S-102 42 STOCKHOLM Facsimile No. +46 8 666 02 86	Authorized officer Yvonne Siösteen/EÖ Telephone No. +46 8 782 25 00

Form PCT/ISA/210 (second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/DK 99/00678

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	PROTEINS: Structure, Function, and Genetics, Volume 26, 1996, Sonia Longhi et al, "Dynamics of Fusarium solani Cutinase Investigated Through Structural Comparison Among Different Crystal Forms of Its Variants" page 442 - page 458 -- --------	1-32,34

INTERNATIONAL SEARCH REPORT

International application No.
PCT/DK 99/00678

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).:

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see next sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-32 and 34

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/DK 99/00678

The invention claimed relates to two different inventions :

I. Claims 1-32 and 34 relate to cutinase variants and the use of these variants.
II. Claim 33 relates to a method for detecting cutinase activity in a sample.

Unity of invention exists only when there is a technical relationship among the claimed inventions involving one or more of the same or corresponding "special technical feature" _ i.e. features that define a contribution which each of the inventions make over prior art. (See Annex B to administrative instructions and Rule 13.1).

INTERNATIONAL SEARCH REPORT

Information on patent family members

02/12/99

International application No.
PCT/DK 99/00678

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9009446 A1	23/08/90	NONE	
WO 9414963 A1	07/07/94	AU 5699994 A	19/07/94
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		EP 0839186 A	06/05/98
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		AU 6655196 A	12/03/97
		CN 1192780 A	09/09/98
		EP 0851913 A	08/07/98
		JP 11510699 T	21/09/99
		WO 9707202 A	27/02/97